

BEST AVAILABLE COPY



MAJORITY	ATGXXGGCGATGCTTCCCTCTTTGAGCCCCAAAGGCCGGGTCTCTCTGGTGACGGGCACCCACCTGGCCT	
DNAPTAQ	...AG..G.....G.....G.....	70
DNAPTFLG.....C..G.....	67
DNAPTTH	...GA.....G.....A.....	70
MAJORITY	ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCCACCOCGGGGGGAACCGGTGCAGGGGCTACGGCTT	
DNAPTAQCA.....G.....G.....	140
DNAPTFLT.....C.....C.....C..T.....	137
DNAPTTHG.....G.....	140
MAJORITY	CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGGACXXGCCGGTGXTCGTGCTTTGACGCCAAG	
DNAPTAQC.....C.....A.....	207
DNAPTFLA.....GT..T.....	204
DNAPTTHT..AA..C..CT.....	280
MAJORITY	GCCCCCTCCTTCGGCCACGAGGCCTACGAGGCCCTACAAGGCGGGCGGGCCCCACCCCCGGAGGACTTTC	
DNAPTAQG..GG.....G.....	277
DNAPTFLG.....G.....	274
DNAPTTHGA.....G.....C.....C.....	280
MAJORITY	CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGACCTCCTGGGGCTTGCGCGCCTCGAGGGTCCCCCGGCTA	
DNAPTAQA.....G.....G.....G.....	347
DNAPTFLG.....T.....A..C.....T...G..G.....T.....	344
DNAPTTHT.....T..A..C.....	350

FIG. 1A

MAJORITY	CGAGGCGGACGACGTXCTGGCCACCCCTGGCCCAAGAGGCGGAAAGGAGGGGTACGAGGTGCGGCATCCTC	
DNAPTAQC.....G.....C.....C.....	417
DNAPTFL	T.....G.....CG.....	414
DNAPTTHT..C.....	420
MAJORITY	ACCGCCGACCGGACCTCTACCAGCTCCTTTCCGACCCGCATCGCCGTCTCCACCCCGAGGGGTACCTCA	
DNAPTAQAAA.....T.....CA.....	487
DNAPTFL	..T.....G.....G.....A.....T.....G.....	484
DNAPTTHA..G.C.....G.....CC.....	490
MAJORITY	TCACCCCGGCGTGGCTTTGGGAGAGAGTACGGCCTGAGGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC	
DNAPTAQC.....A.....C..C.....CC.....A..	557
DNAPTFLAC.....C.C.....T..C.....C.T	554
DNAPTTHA.....C.....T.....C.....	560
MAJORITY	GGGGGACCCCTCCGACAACCTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG	
DNAPTAQ	C.....GAG.....T.....G..GAG.....T..GG..	627
DNAPTFLG..T...A.....G.....A..G...A..CGC	624
DNAPTTHTC.....A..	630
MAJORITY	GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAAGCCCGC...CXTCCGGGAGAGA	
DNAPTAQGC.....C.....A.....	694
DNAPTFLT..C..C.....A.....T....T.G.....C	691
DNAPTTHA.....A.....A.AAAA.G.....	700

FIG. 1B

FIG. 1C

FIG. 1C

MAJORITY	CGGGGXCTCCTCGCCCAAGGACCTGGCCGTTTTTGGCCCTGAGGGAGGGGCTXGACCTCXTGCCCCGGGGACG	
DNAPTAQG..T.....A.....AG.....C.....A.....T.G.....CC.....C.....	1114
DNAPTFLAA.....G.....G.....C.....G.....T.C..A.A.....	1111
DNAPTTHC.....C.....C.....TC.....G..A.....G.....	1120
MAJORITY	ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACACCACCCCGAGGGGGTGCCCGCGCTACGG	
DNAPTAQT.....	1184
DNAPTFLG.....T.....T.....T.....	1181
DNAPTTHG.....	1190
MAJORITY	GGGGGAGTGGACGGAGGAXGCGGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGGAG	
DNAPTAQ	C.....G.....GC.....T.....GCC.....GTG..G..	1254
DNAPTFLT.....A.....GG.....C.C.....A..C...AAA....	1260
DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY	CGCCTTGAGGGGGAGGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAGCCCCCTTTCCCGGGTCCIGG	
DNAPTAQ	A.G.....G.....G.....G.....GCT.....	1324
DNAPTFLA...A..A..C.C..G.....G.....G.....GT...	1321
DNAPTTHC.....A.....C.....C.....A.....C.....	1330
MAJORITY	CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA	
DNAPTAQG..C.....T...AG...T.G.....C...	1394
DNAPTFLGG.....C.....C.....A..C	1391
DNAPTTHC.....A.....T.....T.....C.T.....	1400

FIG. 1D

MAJORITY	GGAGATCCGCCGCTCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCCGGGAC	
DNAPTAQGC.....CC.....	1464
DNAPTFLG.G....AG..G.....	1461
DNAPTTHT.....G.....	1470
MAJORITY	CAGCTGGAAAGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC	
DNAPTAQC.....A.....	1534
DNAPTFLGC.....G.C..G..T.....	1531
DNAPTTHTA.....T.G..G.....C.A.....	1540
MAJORITY	GCTCCACCAGCGCCGCTGCTGGAGGCCCTXCGXGAGGCCACCCCATCTCGTGGAGAAGATCCTGCAGTA	
DNAPTAQC.....C..C.....	1604
DNAPTFLT.....G..A.....CCGC.....	1601
DNAPTTHG.....A..G.....C...C..	1610
MAJORITY	CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCCXGXCCCTCGTCCACCCACGGACGGGC	
DNAPTAQG....G.....T.....T....G.A...A.....	1674
DNAPTFLA.....A.....C.C...G.....A...C...	1671
DNAPTTHG.G.....AAG.....G.....	1680
MAJORITY	CGCCTCCACACCCGCTTCAACCAGACGGCCACGGGCACGGCAGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQA.....A.....T.....C..	1744
DNAPTFL	..G.....C.....TCC.....	1741
DNAPTTHG.....G.....	1750

FIG. 1E

MAJORITY AGAACATCCCCGTCCGCACCCXCTGGGCCAGAGGATCCGCCGGGCCTTCGTGGCCGAGGAGGGXTGGGT

DNAPTAQG..T..G.....A.C.....G...C. 1814
 DNAPTFLG.....C.C.....A.....C..... 1811
 DNAPTTHCT.....C...T....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCTGGCCCCACCTCTCCGGGGACGAGAACCTG

DNAPTAQ A.....A.....A...G.....C..... 1884
 DNAPTFL .C.....T.T.....C.....T..... 1881
 DNAPTTHC.....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGGAGGACATCCACACCCAGACCCGCGAGCTGGATGTTCCGGCGTCCCCCGG

DNAPTAQC.....C.....GG.....G... 1954
 DNAPTFLT.....T.....TT...C. 1951
 DNAPTTH ...A.....A.....A..... 1960

MAJORITY AGGCCGTGGACCCCTGATGCGCCGGCGGCCAAGACCATCAACTTCGGGGTCTCTACGGCATGTCCGGC

DNAPTAQA.GG..A....T.....GG.G.....C.....G... 2024
 DNAPTFLA.GG..A....T.....GG.....G..... 2021
 DNAPTTHA.GG..A....T.....GG.....C..... 2030

MAJORITY CCACCGCCTCTCCAGGAGCTTGCCATCCCCCTACGAGGAGGCGGTGGCCTTTCATTGAGCGCTACTTCCAG

DNAPTAQA.....A.....T.....CCA.....T... 2094
 DNAPTFLGG.....T..... 2091
 DNAPTTH ...TA.G.....T.A.....A 2100

FIG. 1F

MAJORITY	AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAGACCTCTGGAGGAGGGCAGGAGCGGGGGTACGTGGAGA	
DNAPTAQ	2164
DNAPTFL	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTHA.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTCGGCCGCGGCTACGTGCCCCGACCTCAACGCCCGGGTGGAAGAGCGTGCGGGAGGCGGCGGA	
DNAPTAQC.....A.....AG.G.....C.....C..	2234
DNAPTFLT.....C.....C.....	2231
DNAPTTH	...AA.AA.....CA.....C.....	2240
MAJORITY	GCGCATGGCCCTTCAACATGCCCGTCCAGGGCACCCGCCCGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAQT.....T.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTHC.....	2310
MAJORITY	TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCTCGAGGCC	
DNAPTAQ	...A...GG.....T.....	2374
DNAPTFL	...T...C.....G...TT.G.....G.....	2371
DNAPTTH	...C.C.G...G.....C.C.....CC...G.....	2380
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCCCGCTTTGGCCAAGGAGGTTCATGGAGGGGGTCTATCCCCCTGGCCGT	
DNAPTAQ	.A.....A.....CC.....CGGC.....G.....	2444
DNAPTFL	...G.C.....AG...A.....GG.....CAG..	2441
DNAPTTH	.C...C.....C...A.....G.....C.....AA..C.....C.....	2450

FIG. 1G

MAJORITY	GCCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG	
DNAPTAQA.....GA	2499
DNAPTFLCC.....	2496
DNAPTTHT.....GT...	2505

FIG. 1H

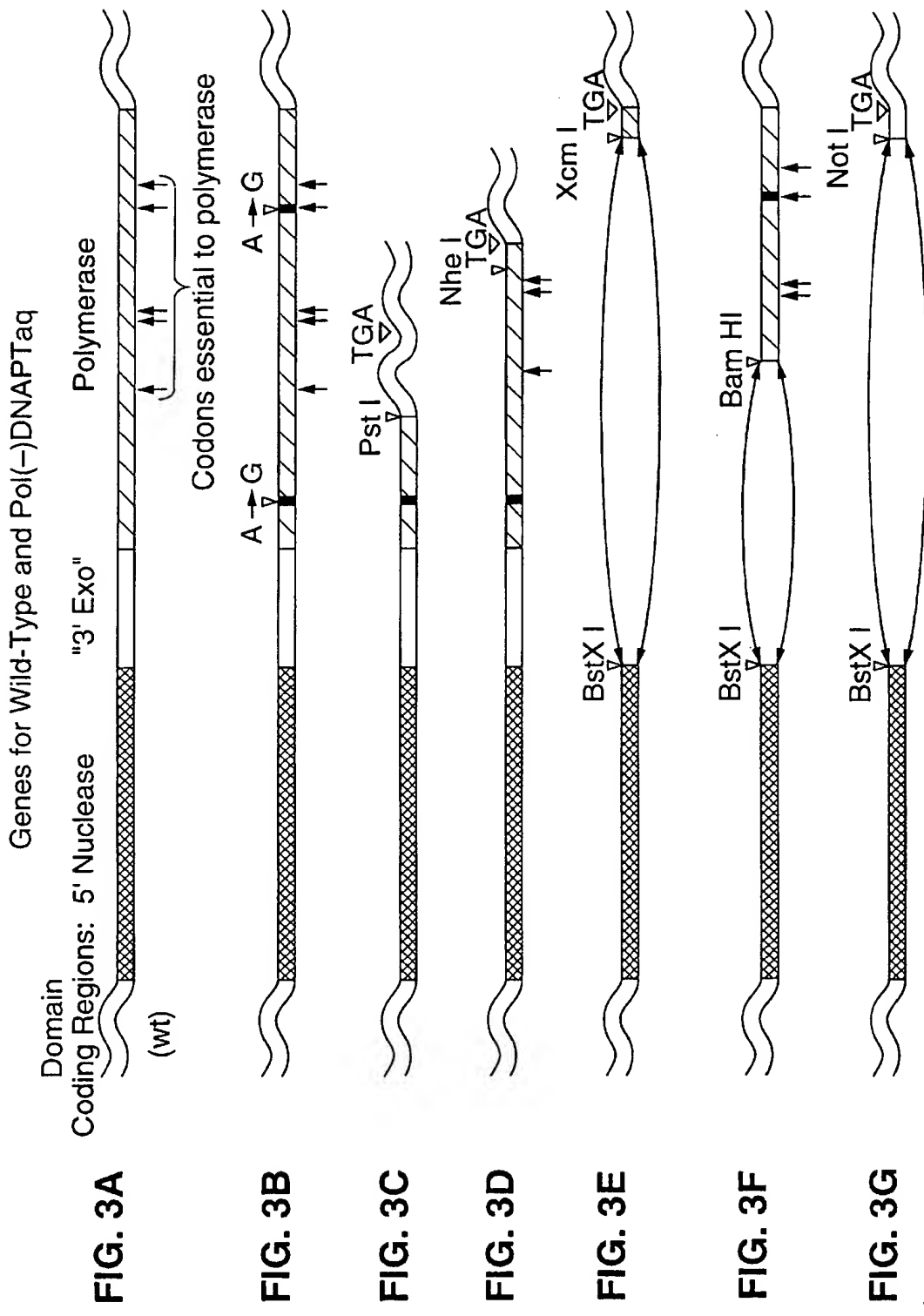
MAJORITY	MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPVQAVYGFAKSLLKALKEDG·DAVXVVVFDK	
TAD PRO	.RG.....H.....	69
TFL PROI.....	68
TTH PROV.V.....	70
	E.....YK..F.....	
MAJORITY	APSRHEAYEAYKAGRAPTEDFPROLALIKELVDLLGLXRLEVPGEADDVLATLAKAEKEGYEVRIL	
TAG PROGG.....A.....S.....	139
TFL PROV.....F.....R.....	138
TTH PROFT.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDNLPGVKGIGECTAXKLLX	
TAG PRO	...K.....H.....D.A...T.E.....R...E	209
TFL PROE..I.....Y.....A.....I.....QR..IR	208
TTH PROV...V.....H.....E.....F...V.....L...K	210
MAJORITY	EWGSLNLLKNLDRVKP·XXREKIXAHMEDLXLSSXLSXVRTDLPLEVDFAXRREPDRGLRAFLERLEF	
TAG PROA.....L...AI...L...D..K..WD..AK.....K.....R.....	278
TFL PROFQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PROENV...K..L...R..LE..R.....L.QG.....	280
MAJORITY	GSLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEALLALAAARXGRVHRAXDPLXGLRDLKEV	
TAG PROS.....K.....D.....PE.YKA.....A	348
TFL PROG...A.....L..SF.....G.WE..L...Q...R.....G.	347
TTH PROA.AP.....K.....C.D.....A...A..K.....	350

FIG. 2A

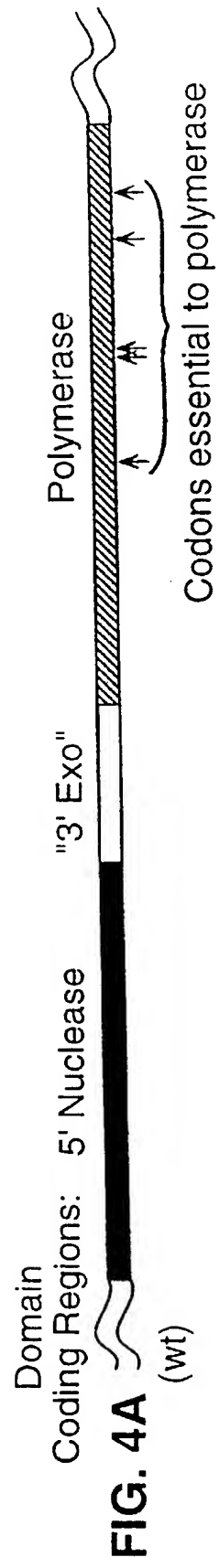
MAJORITY	RGLLAKDLAVLALREGDLXP	GDDPMLLAYLLDPSNTT	PEGVARRYGGWETEDAGERALL	SERLFXNLXX	
TAQ PROS.....	G.P.....E.....	A.....A.....	WG 418
TFL PROI.....F.E.....A.....QT.KE	417
TTH PROS.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEE	IRRL	EEEEV	FRLAGHPFNL	NSRD
TAQ PROR...R...A.....R.....A.....	488
TFL PROK.....E.....EA.V.Q.....	487
TTH PROK.....H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGKTEKTKRSTSA	AAVLEALREAHPIVEKILQYREL	TKLKN	TYIDPLPXLVHPRTG	
TAQ PROS.....D.I.....	558
TFL PRODR.....A...K...	557
TTH PROR...L...Q.....H.....V...S.....	560
MAJORITY	RLHTRFNQTATATGR	LSSDPNLQNI	PVRTPLGQRIRRAFVAEE	GWXLVALDYSQIELRVLAHLSGDENL	
TAQ PROI...L.....	628
TFL PROV...V.....	627
TTH PROA...A.....	630
MAJORITY	IRVFQEGRDIHTQTASWMF	GPPEAVDPLM	RRAAKTINFGVLYGMSA	HLSQLAIPYEEA	FIERYFQ
TAQ PROE.....R.....Q.....	698
TFL PROS...G.....G...S.....	697
TTH PROK.....V.....	700

FIG. 2B

FIG. 2C



Genes for Wild-Type and Pol(-)DNAPTfl



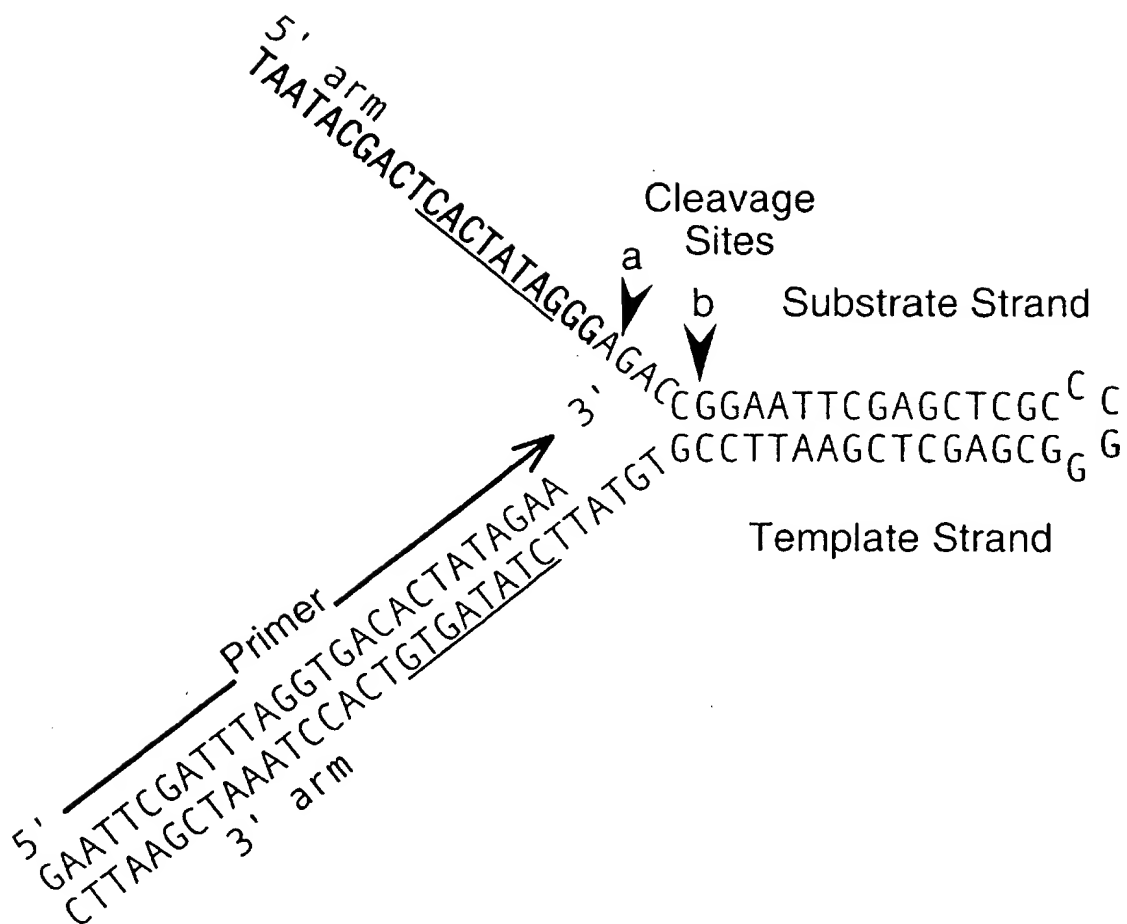


FIG. 5

DNAP
TARGET
DNA

	T		S		
	┌───┐		┌───┐		
M	-	+	-	+	M

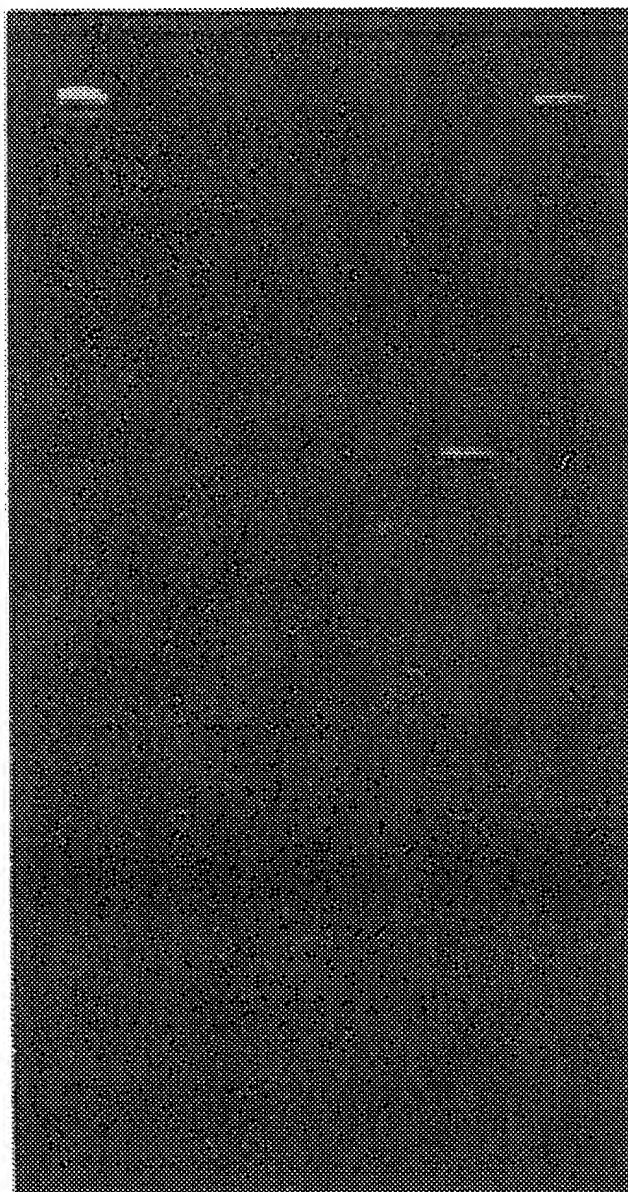


FIG. 6

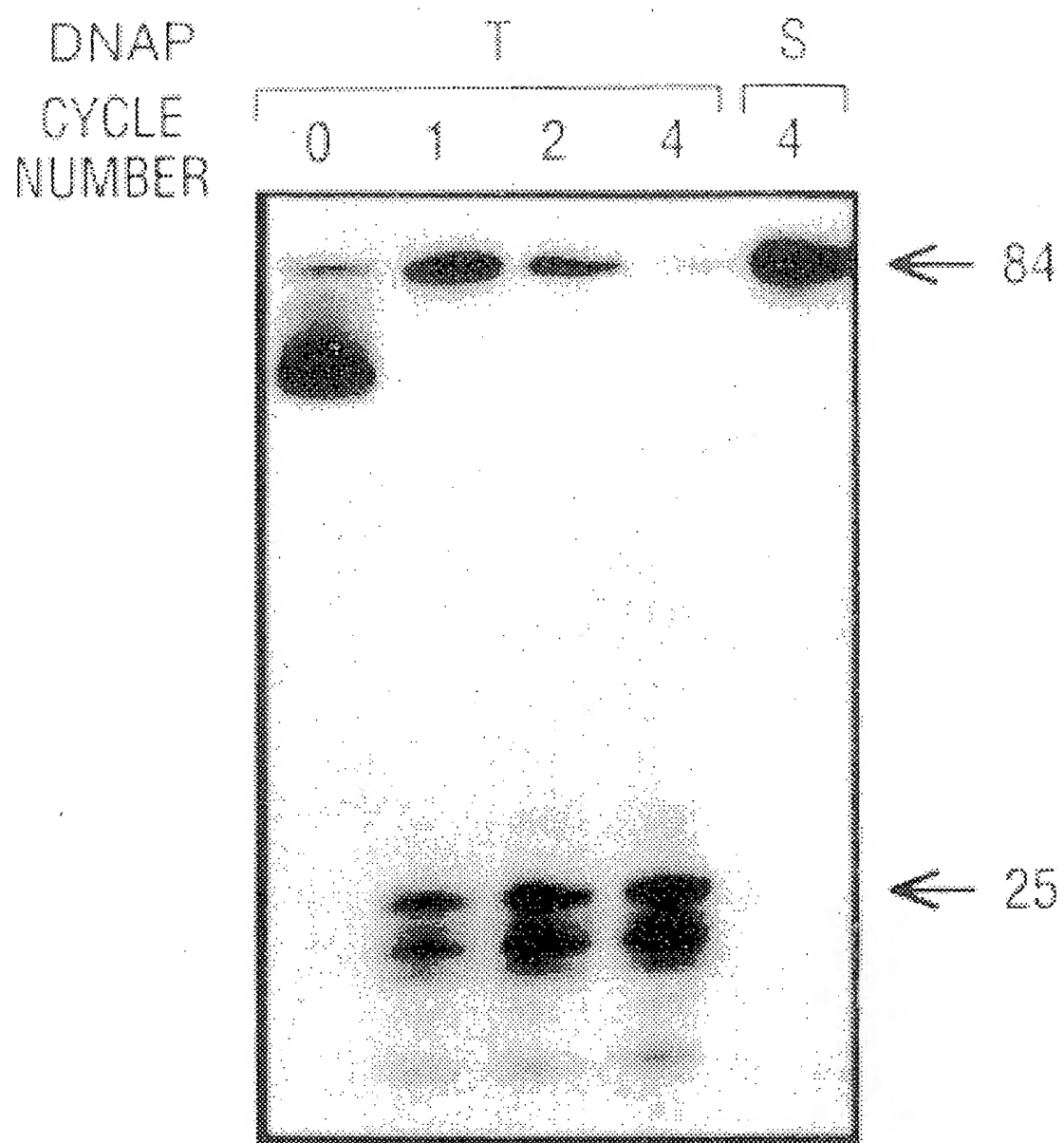


FIG. 7

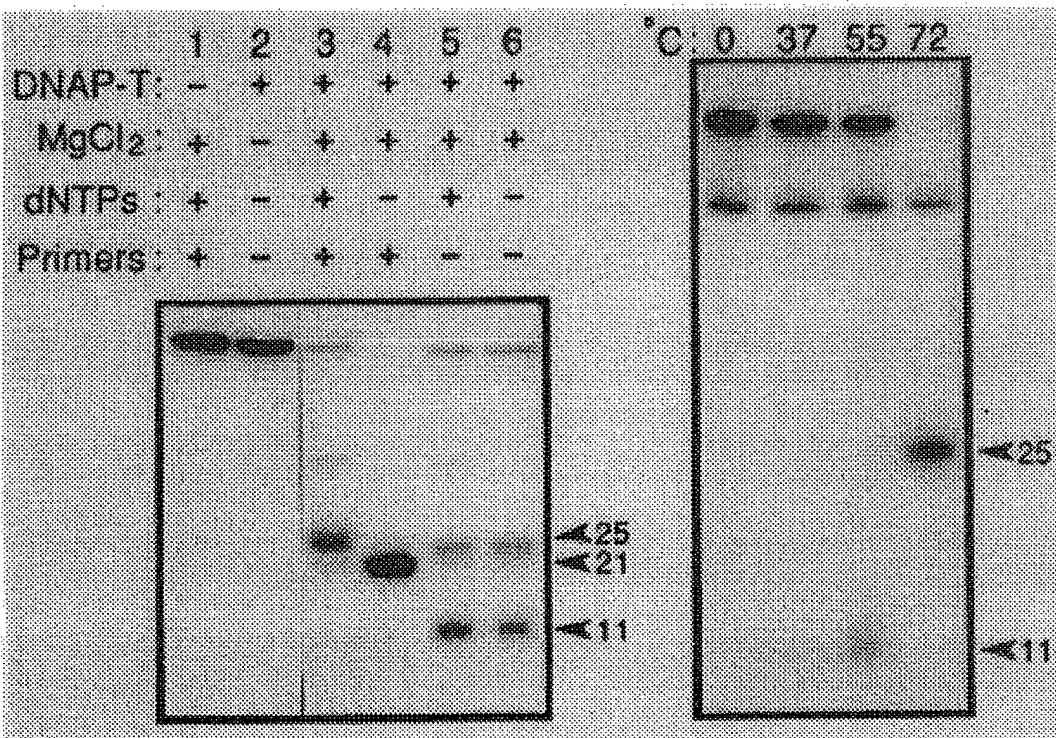


FIG. 8A

FIG. 8B

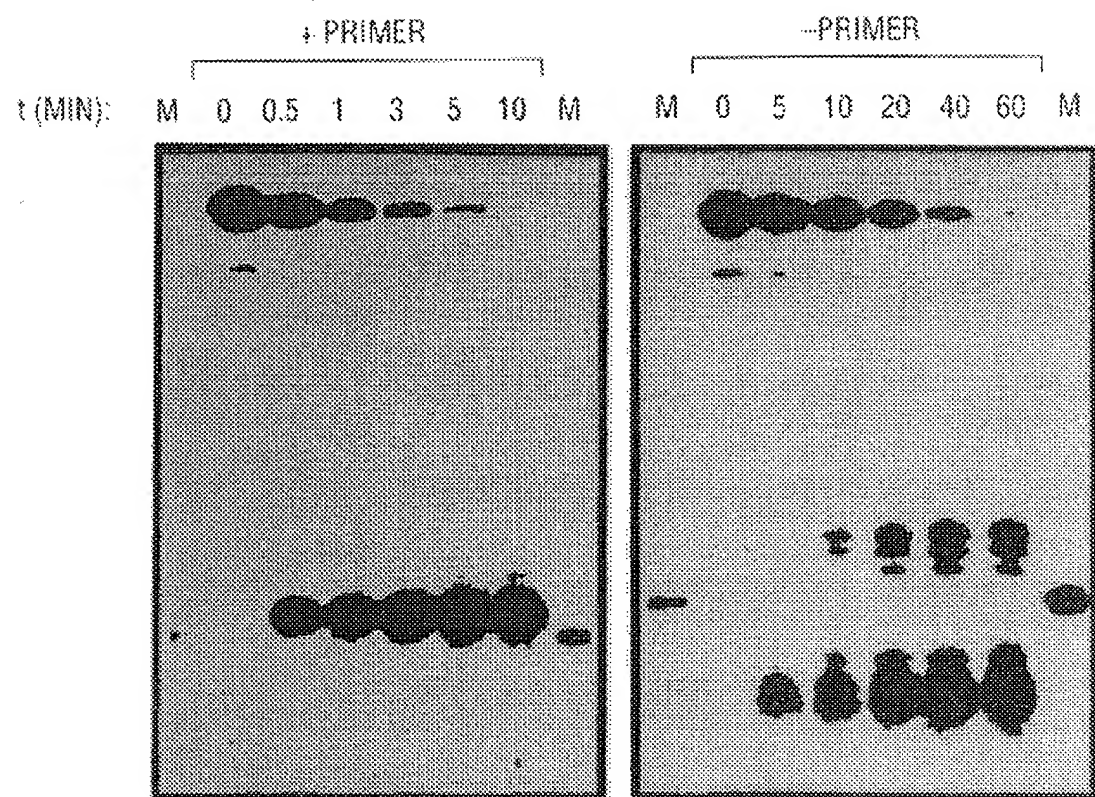
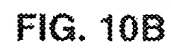


FIG. 9A

FIG. 9B



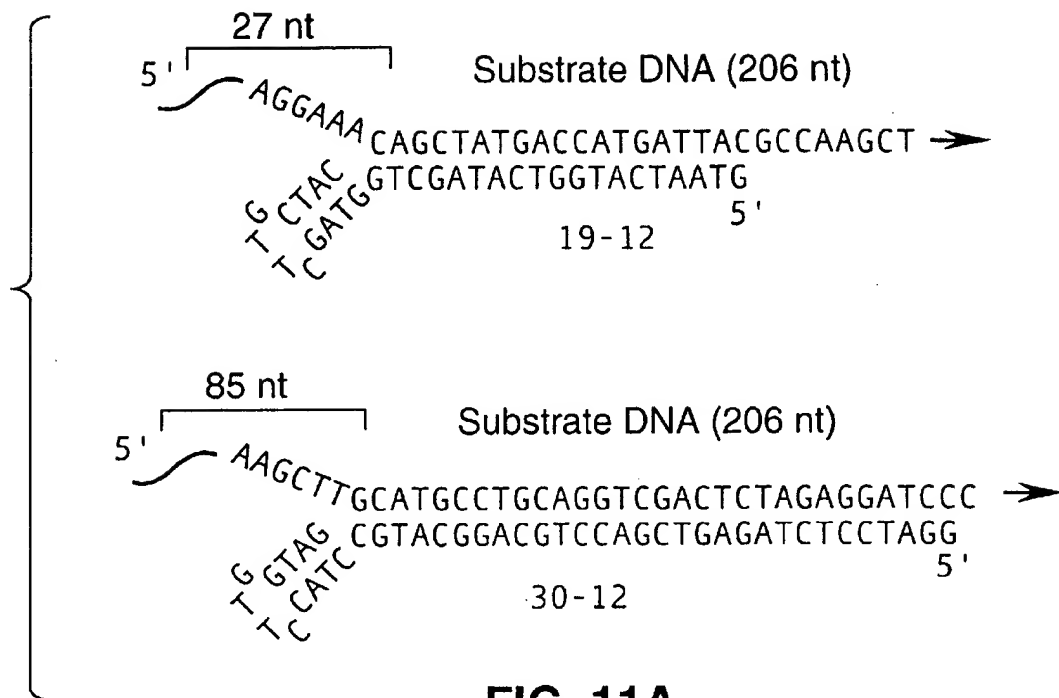


FIG. 11A

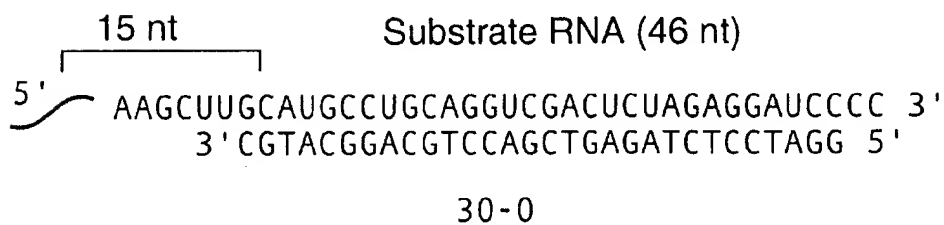


FIG. 12A

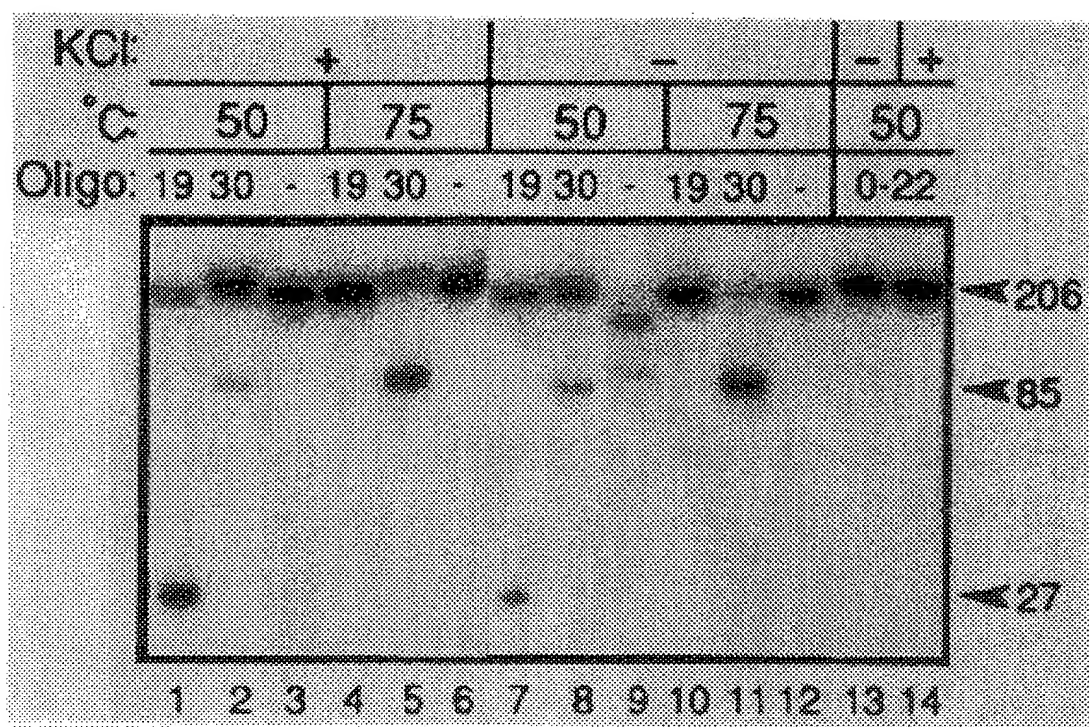


FIG. 11B

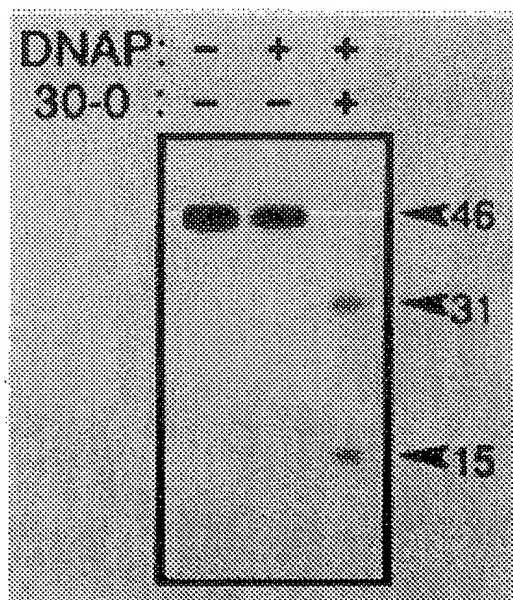
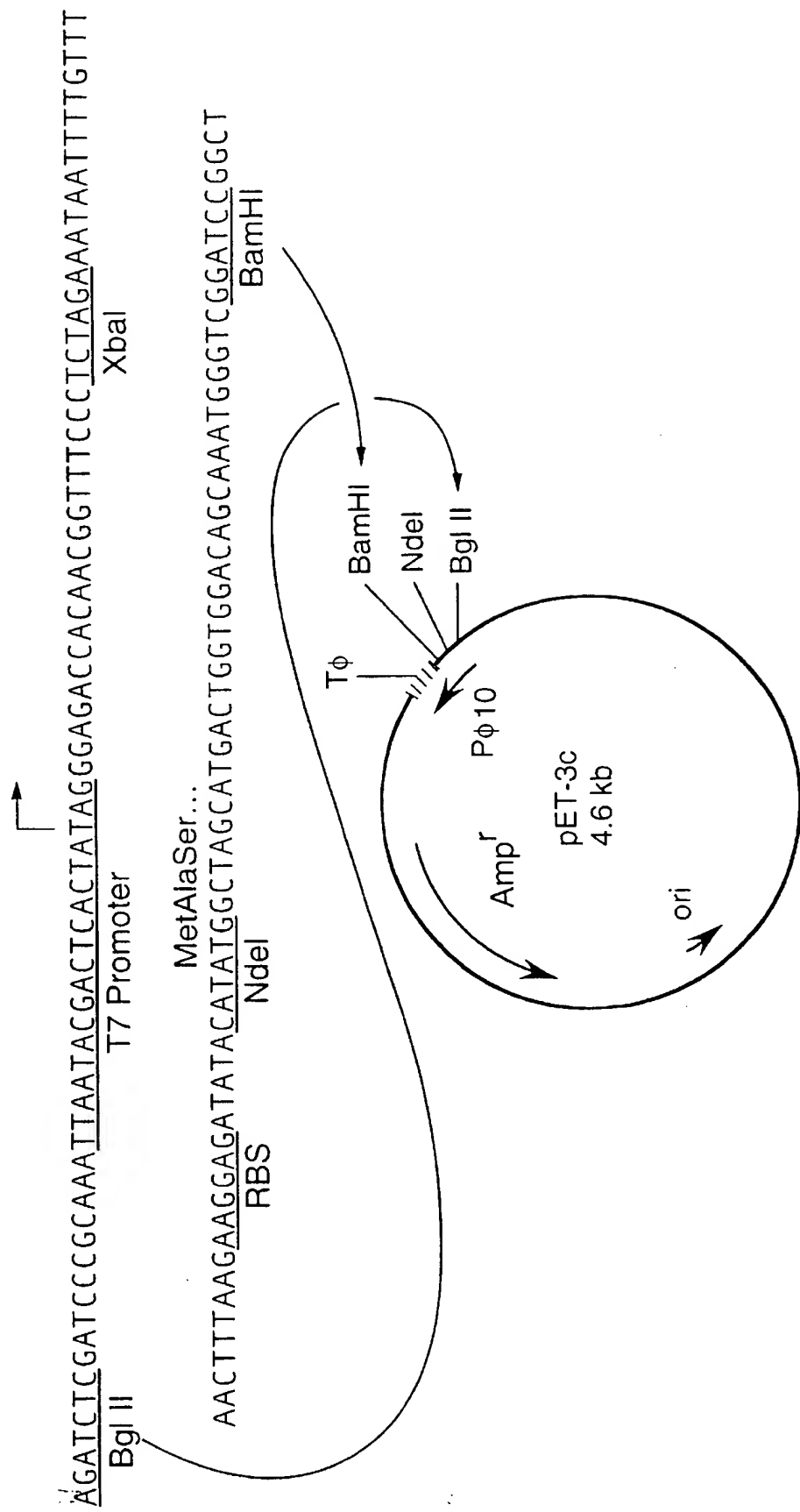


FIG. 12B



P ϕ 10 : Bacteriophage T7 ϕ 10 promoter RBS: Ribosome binding site
 T ϕ : T7 ϕ Terminator

FIG. 14

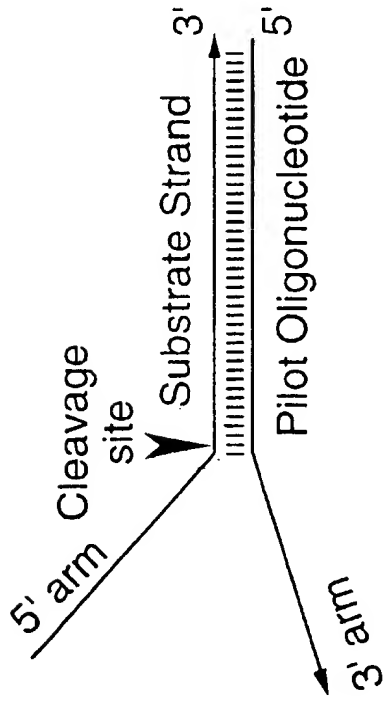


FIG. 15A

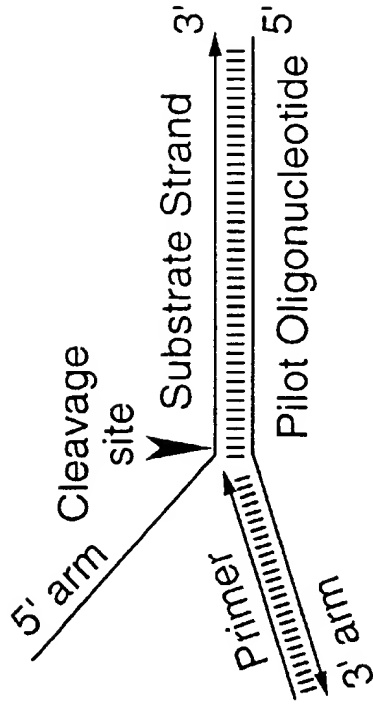


FIG. 15B

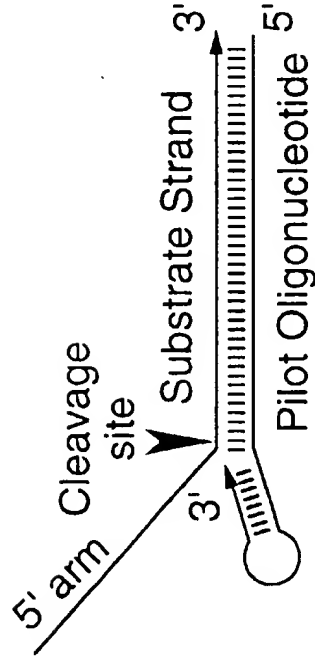


FIG. 15C

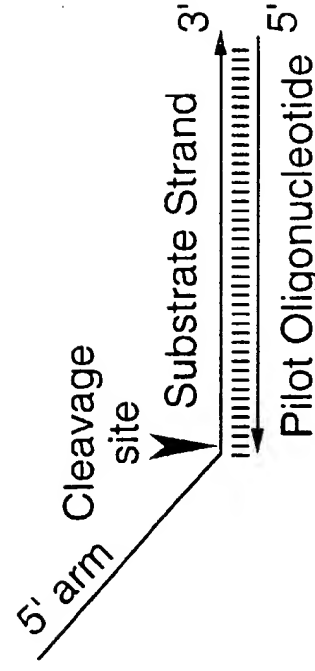


FIG. 15D

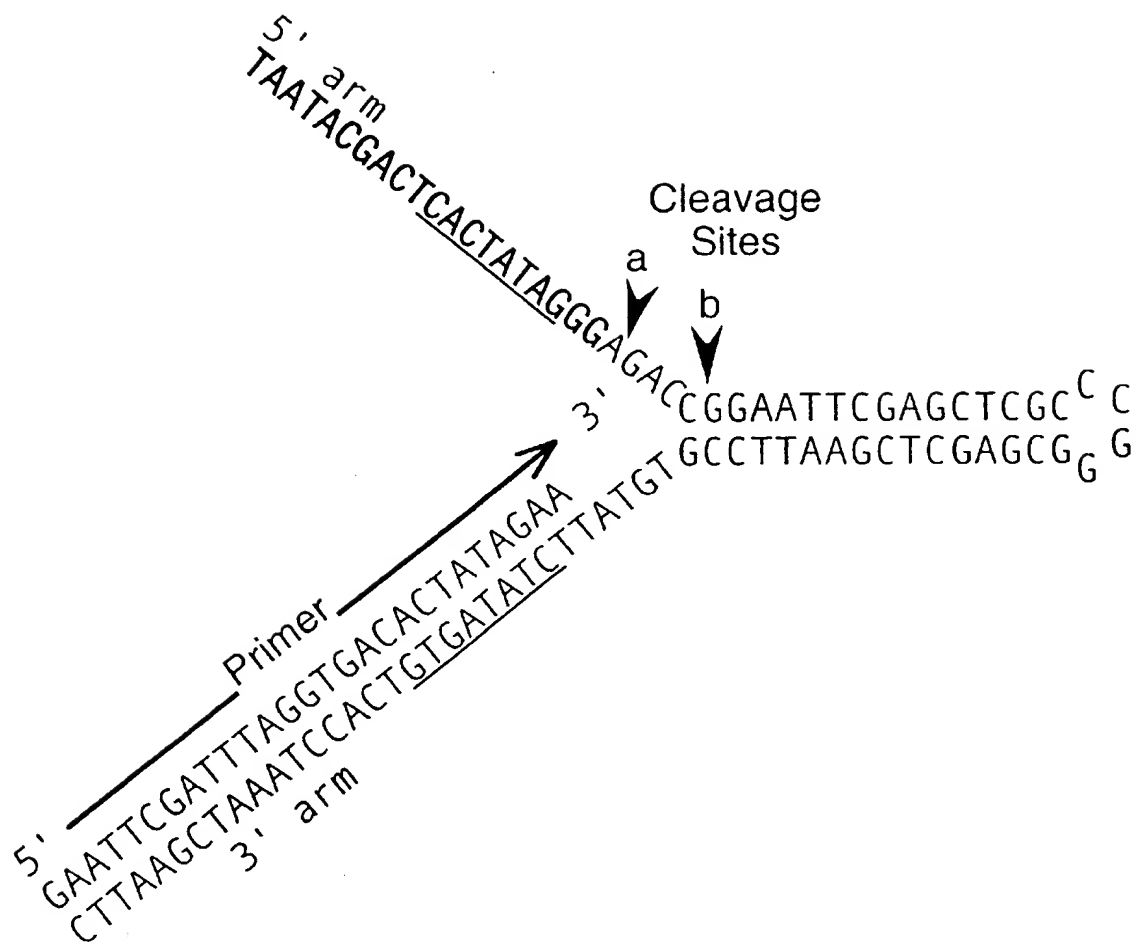
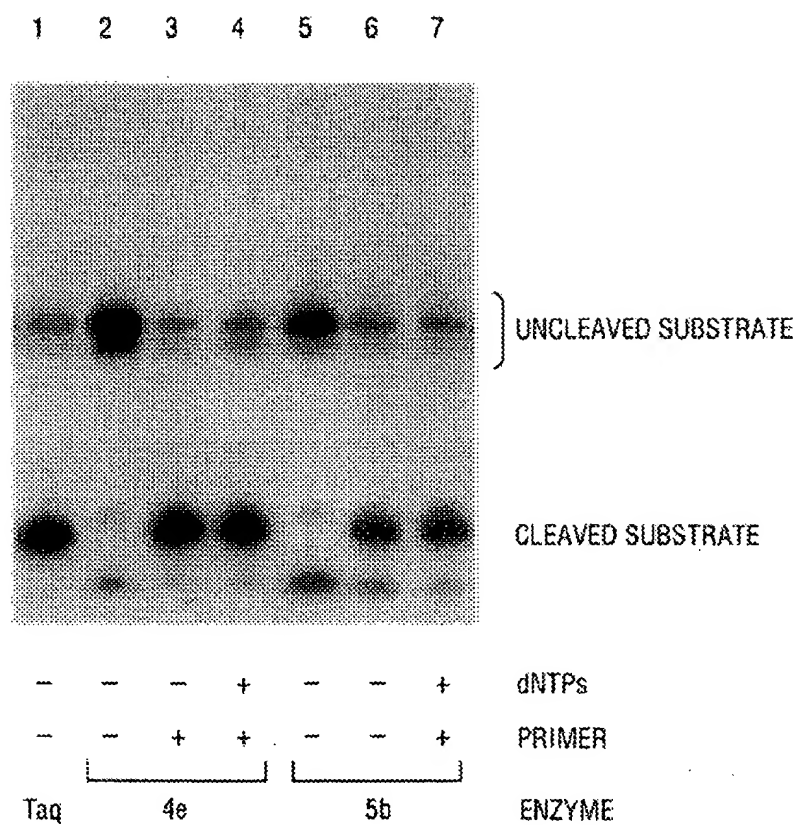


FIG. 15E

FIG. 16



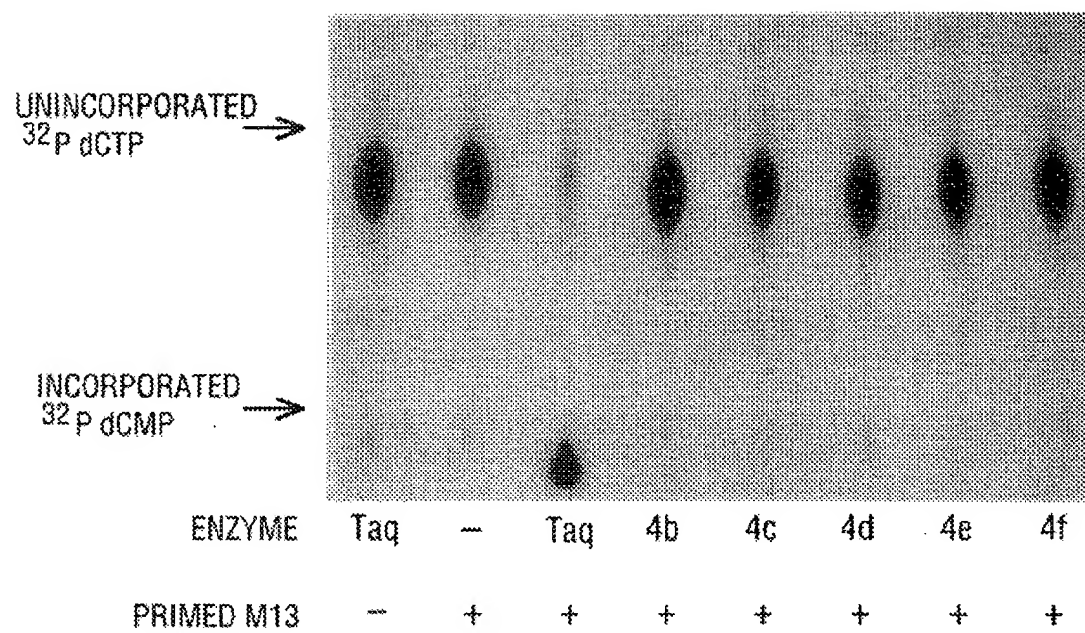


FIG. 17

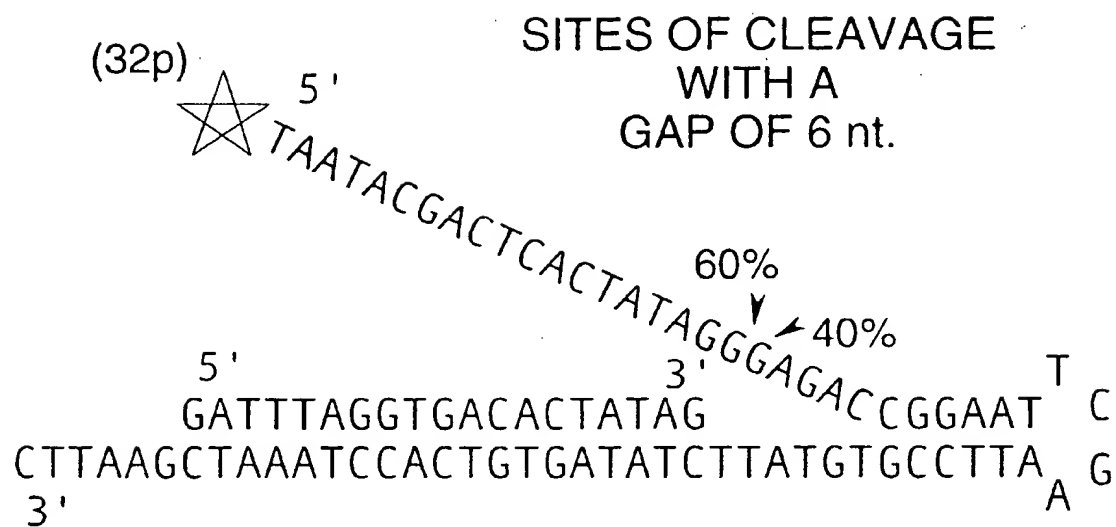


FIG. 18A

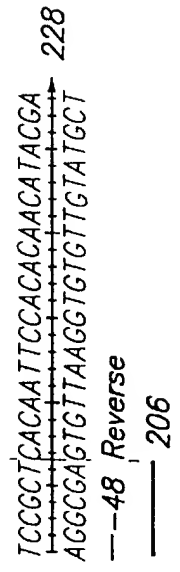
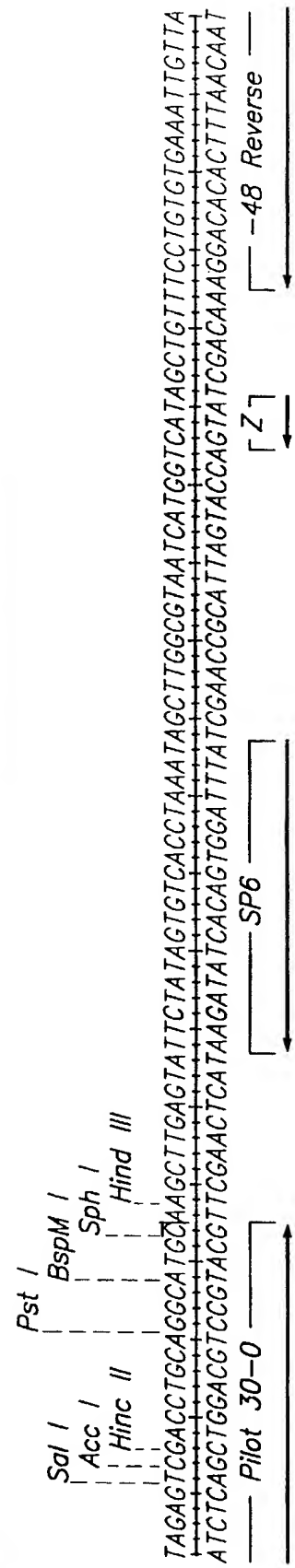
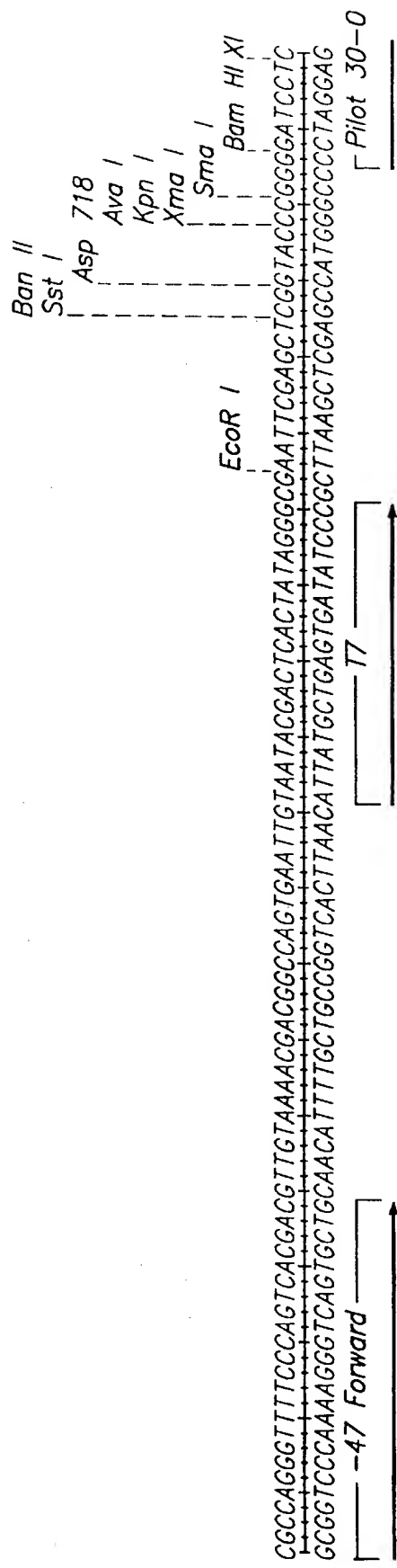


FIG. 19

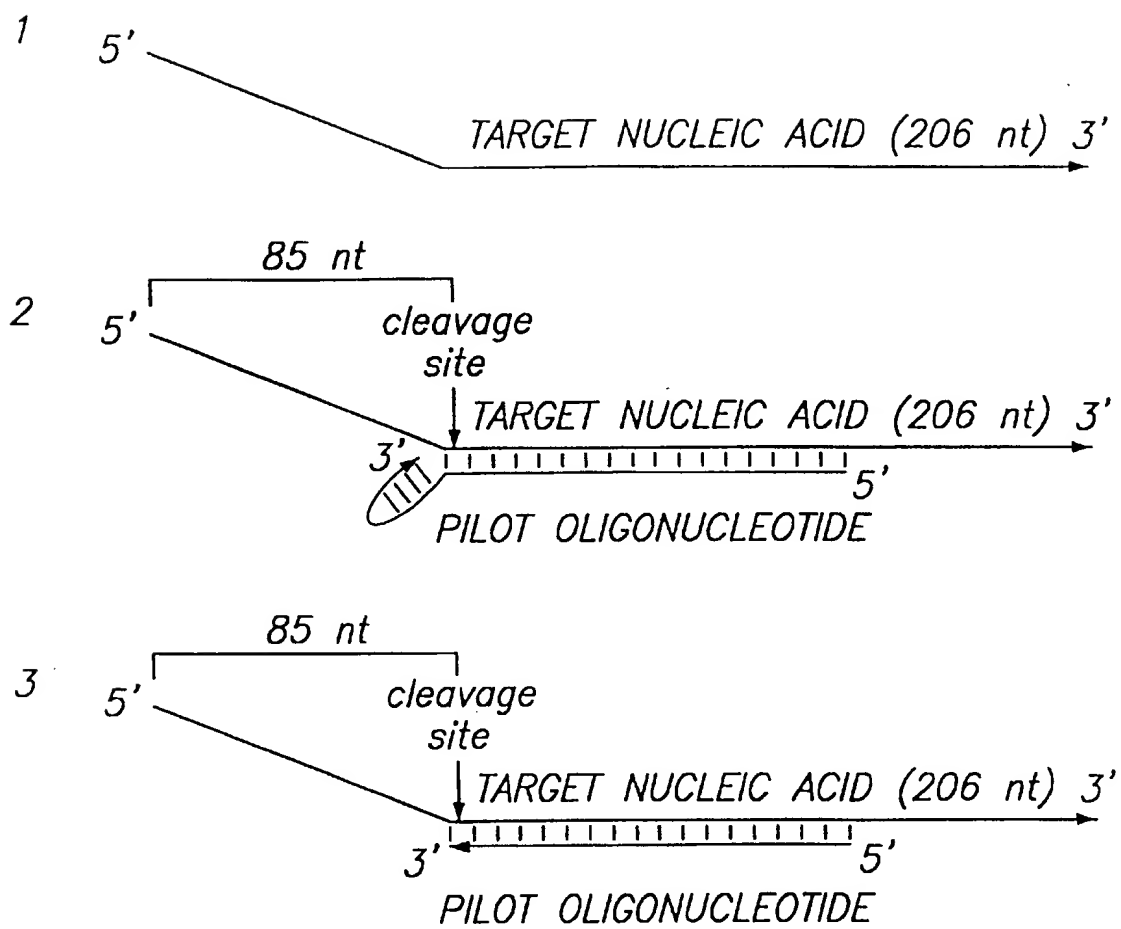


FIG. 20A

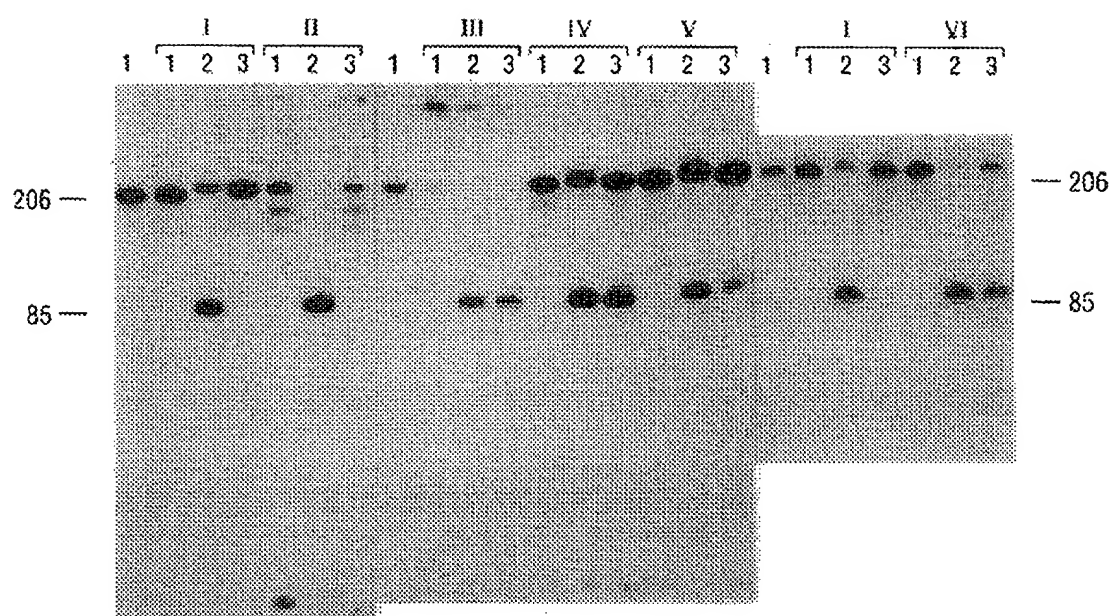


FIG. 20B

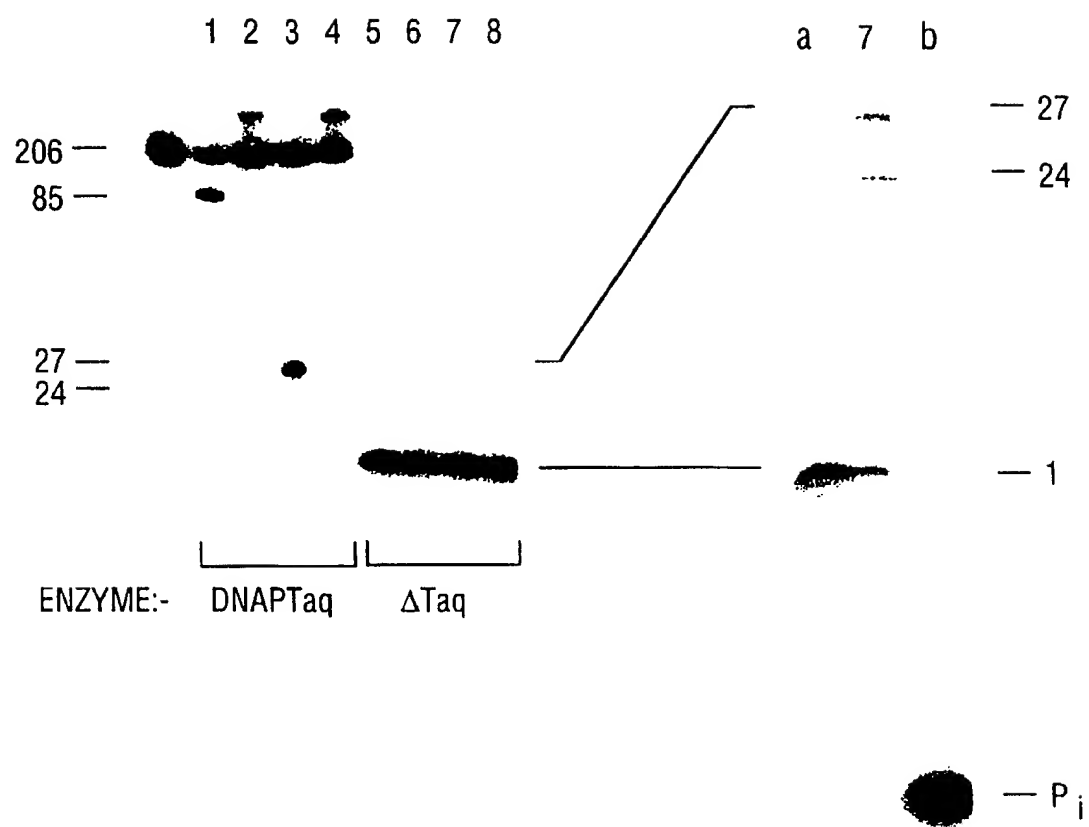


FIG. 21A

FIG. 21B

FIG. 22A

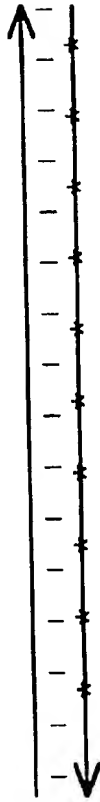
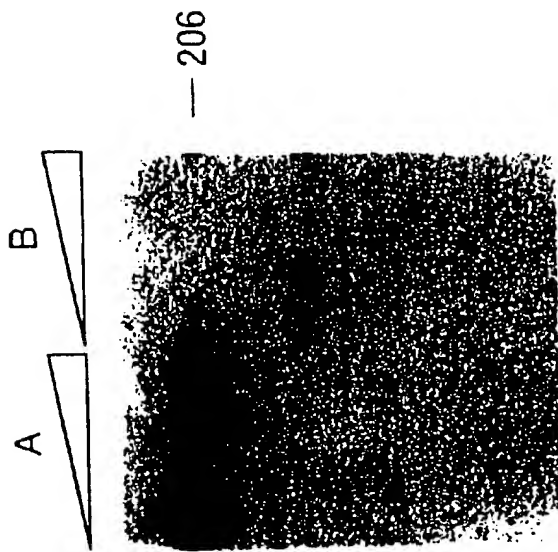


FIG. 22B

* = 32p



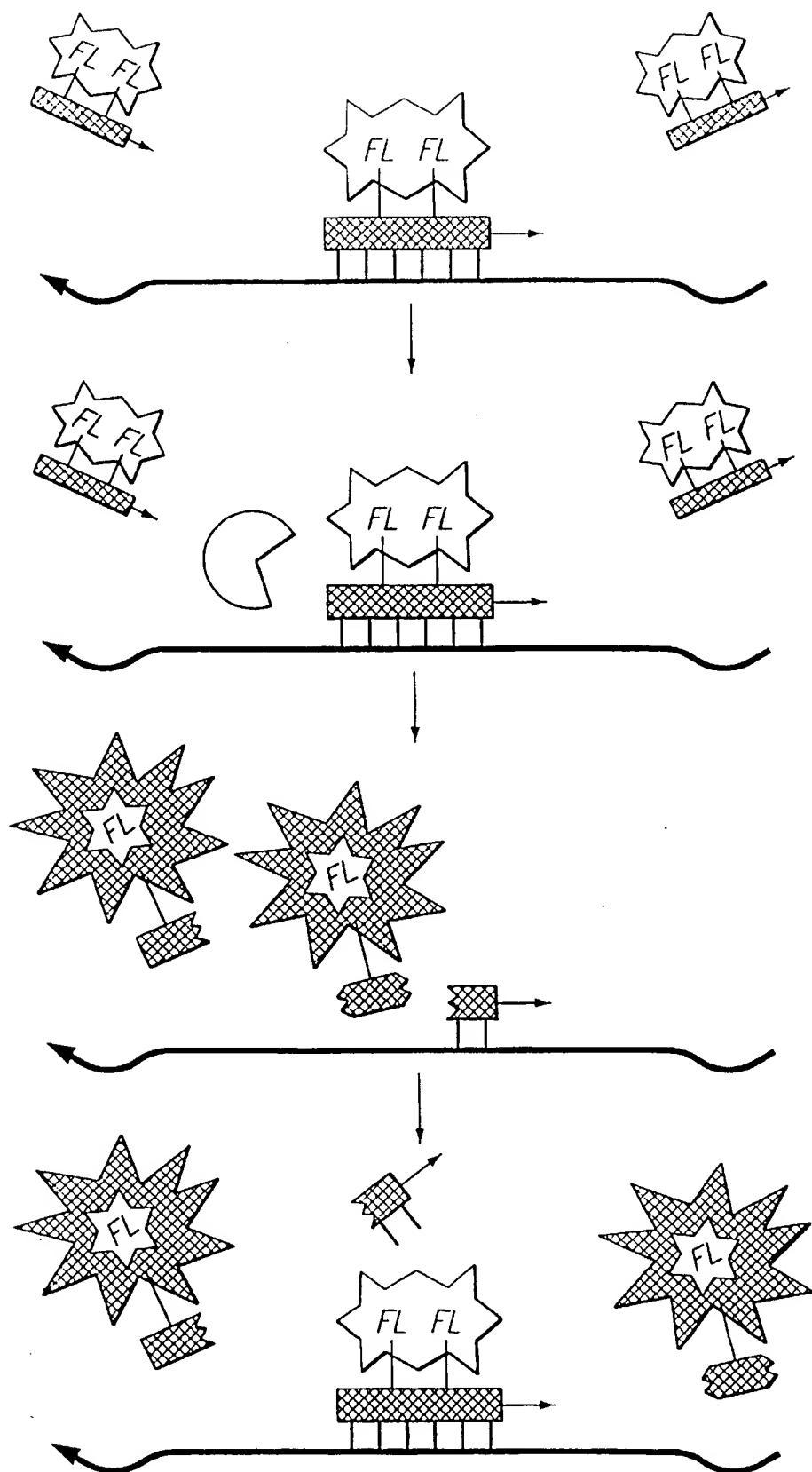


FIG. 23

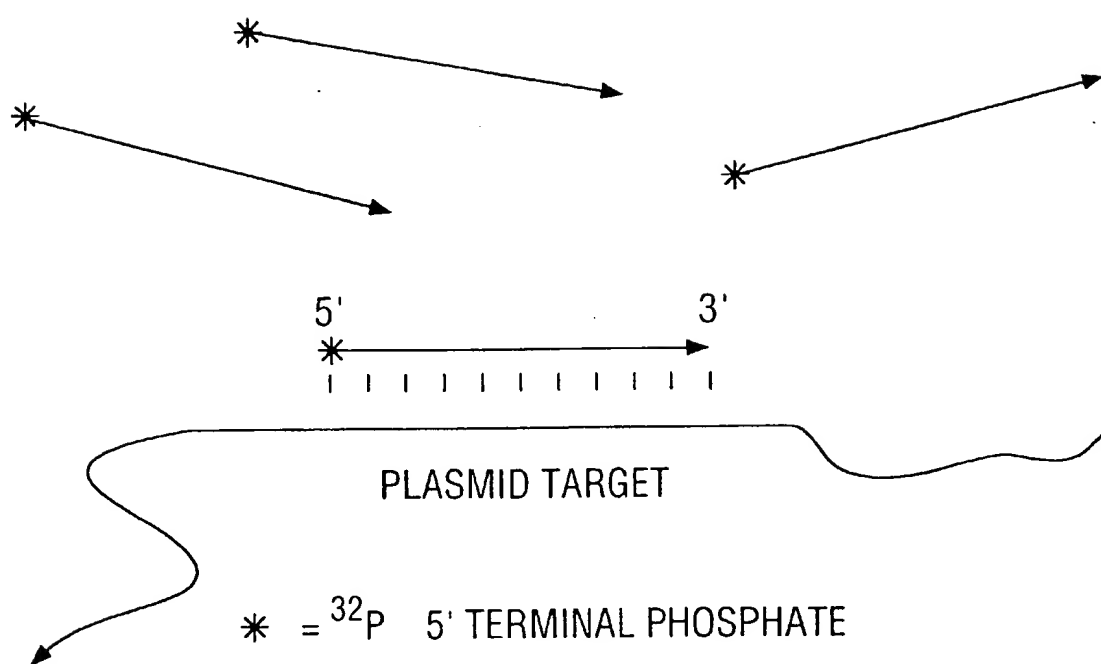


FIG. 24A

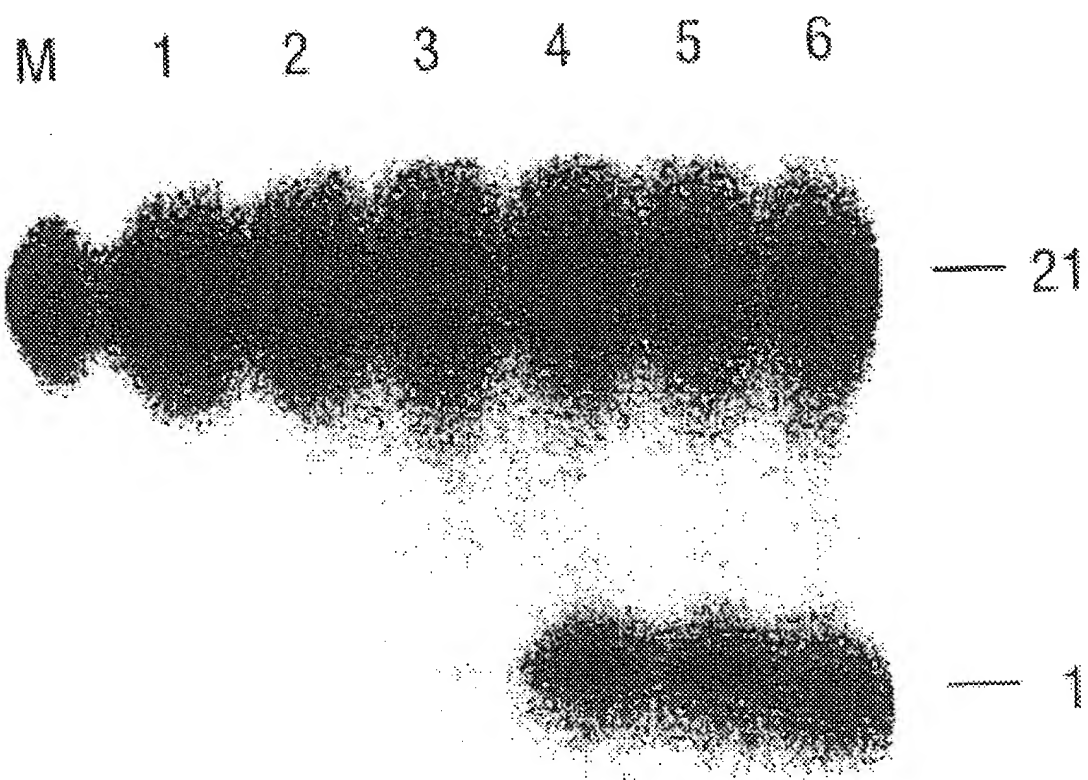


FIG. 24B

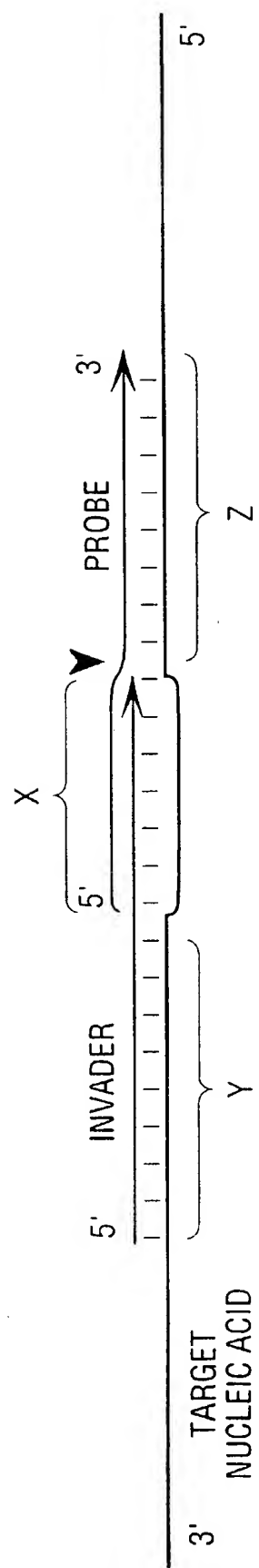


FIG. 25

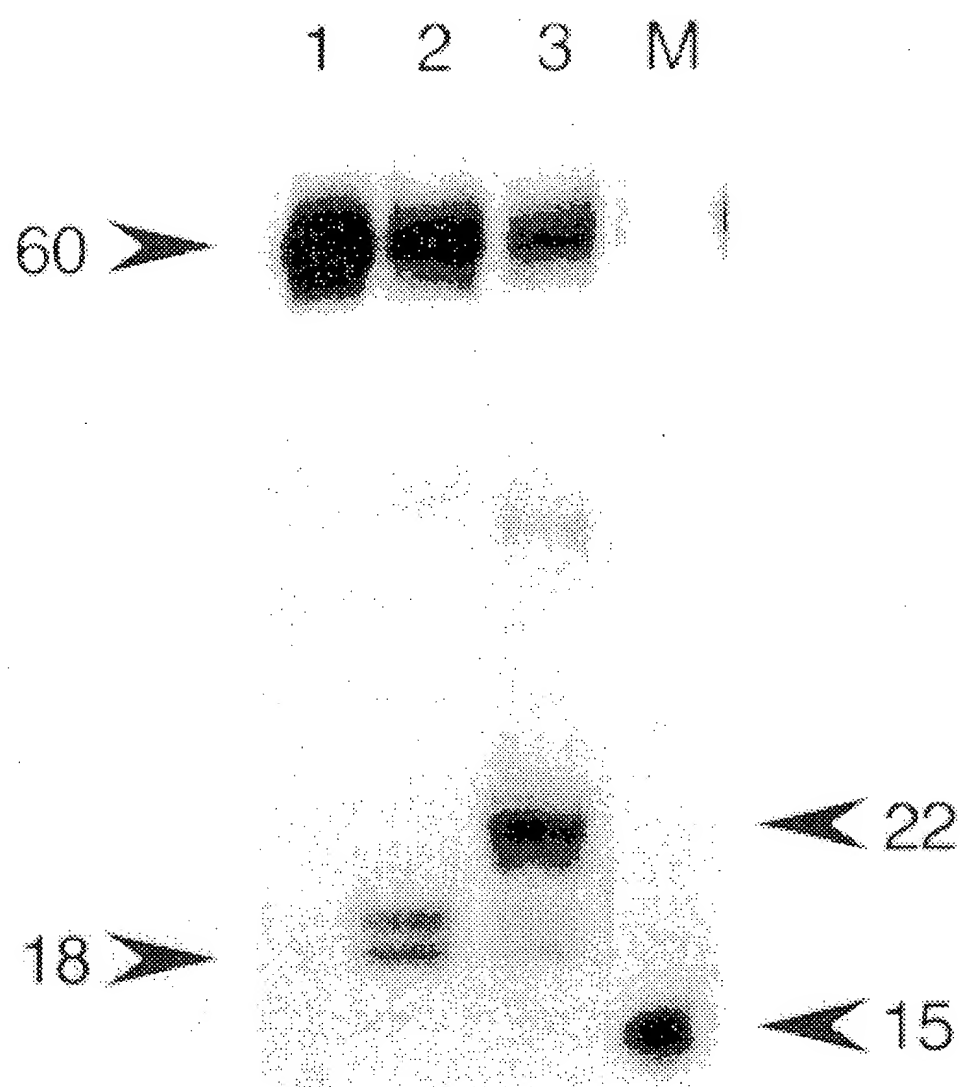


FIG. 27

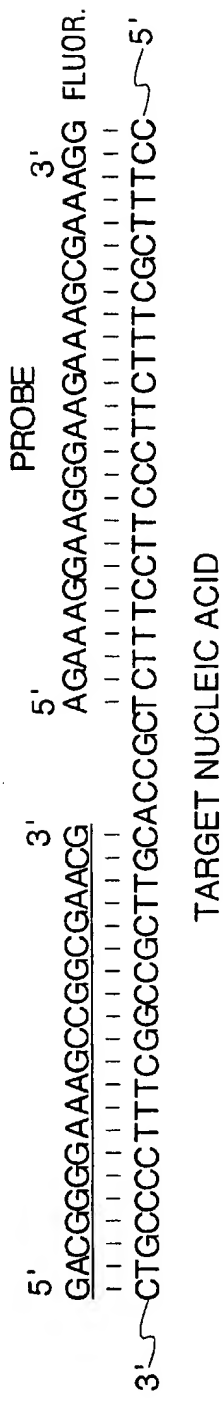


FIG. 28A

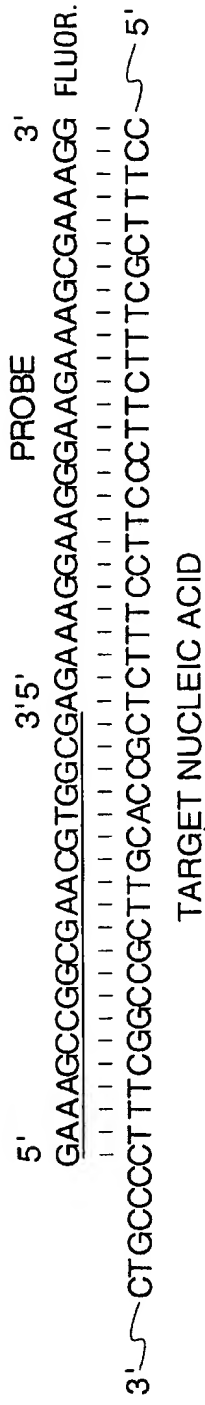


FIG. 28B

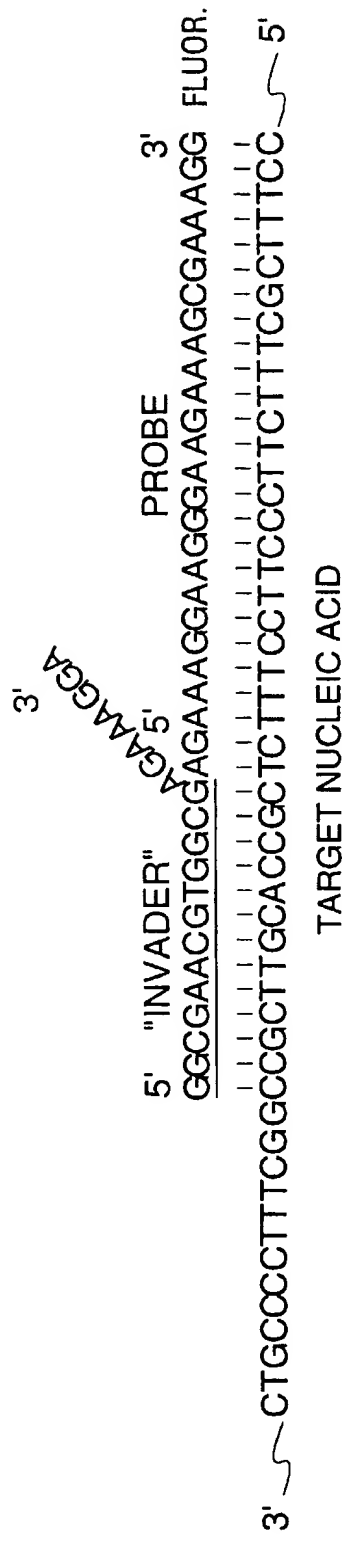


FIG. 28C

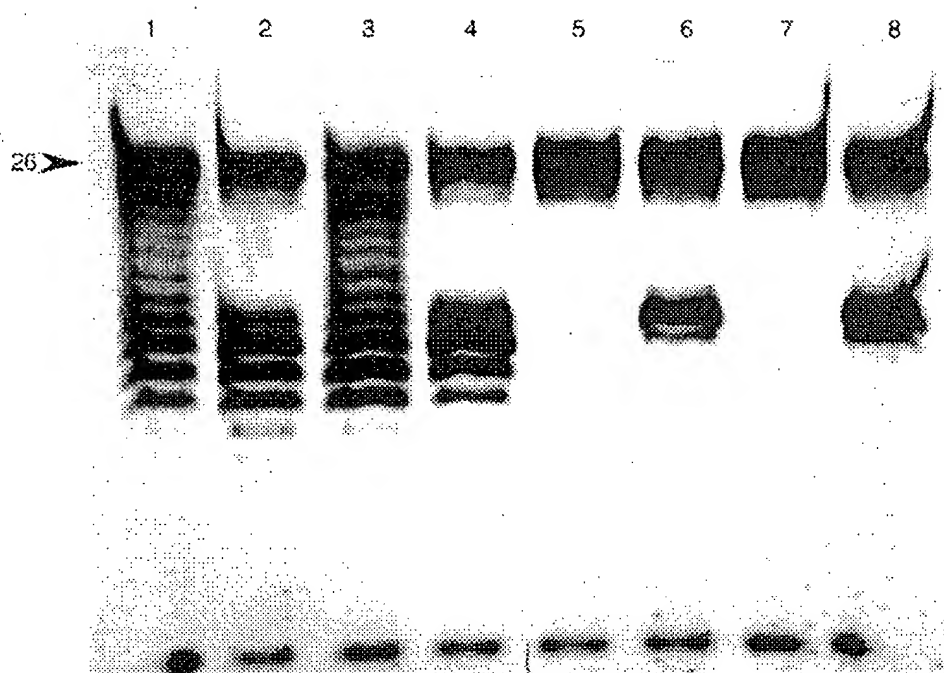


FIG. 29

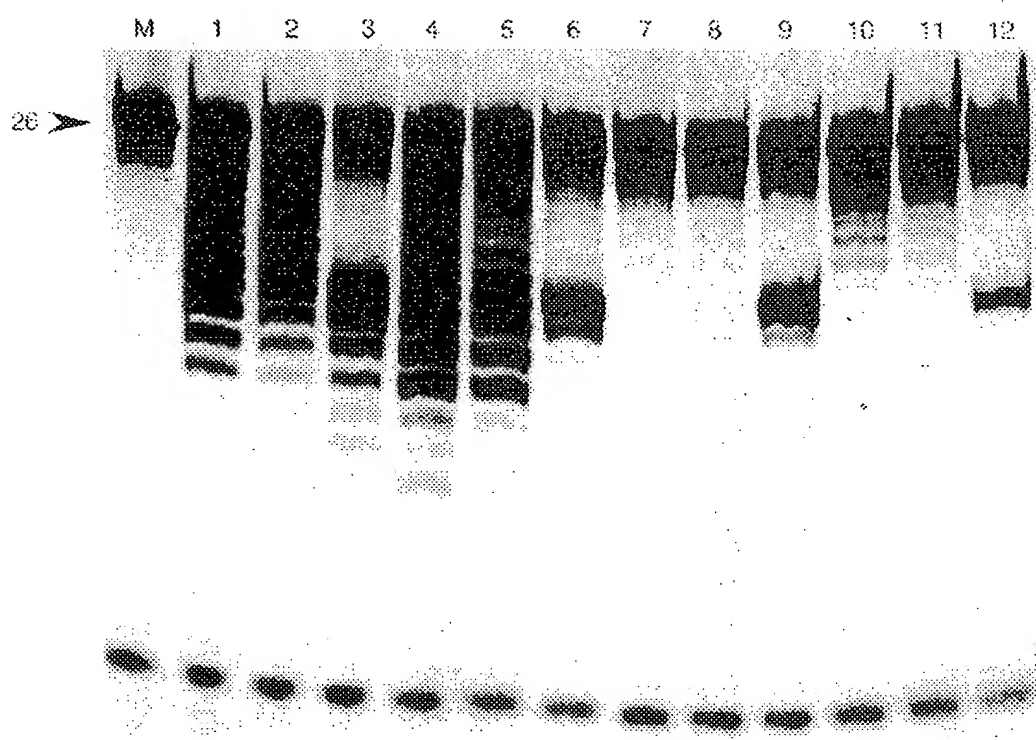


FIG. 30

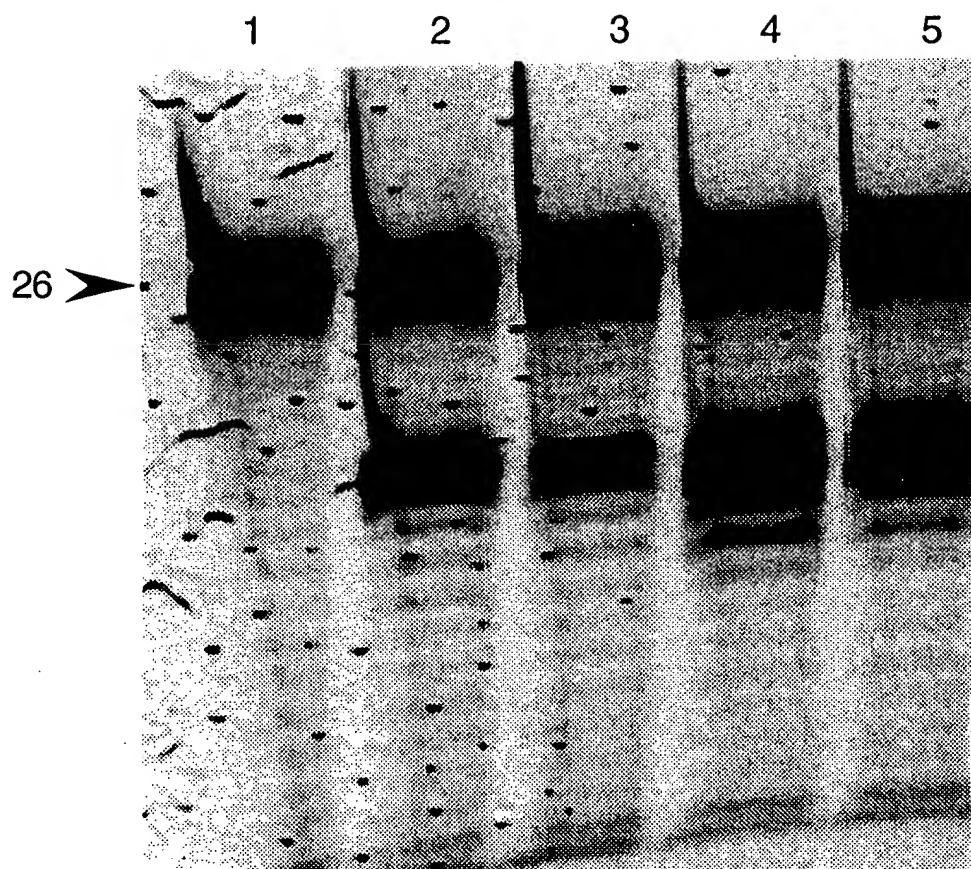


FIG. 31

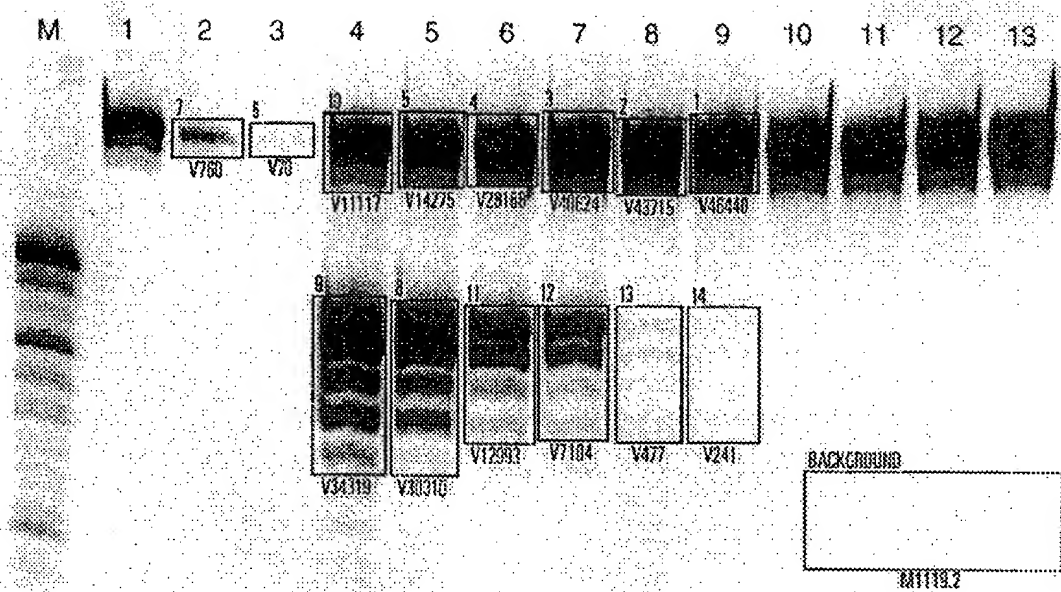


FIG. 32

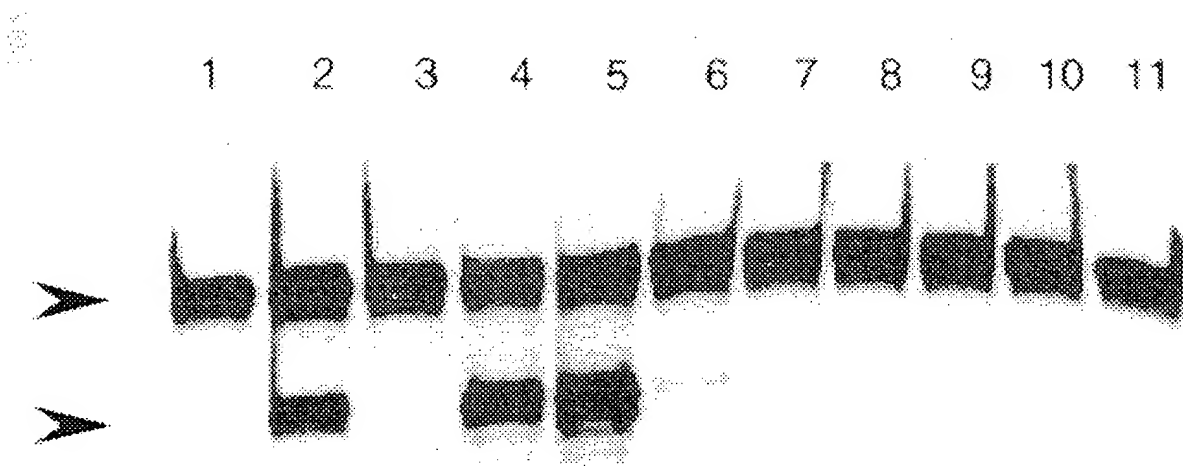


FIG. 33

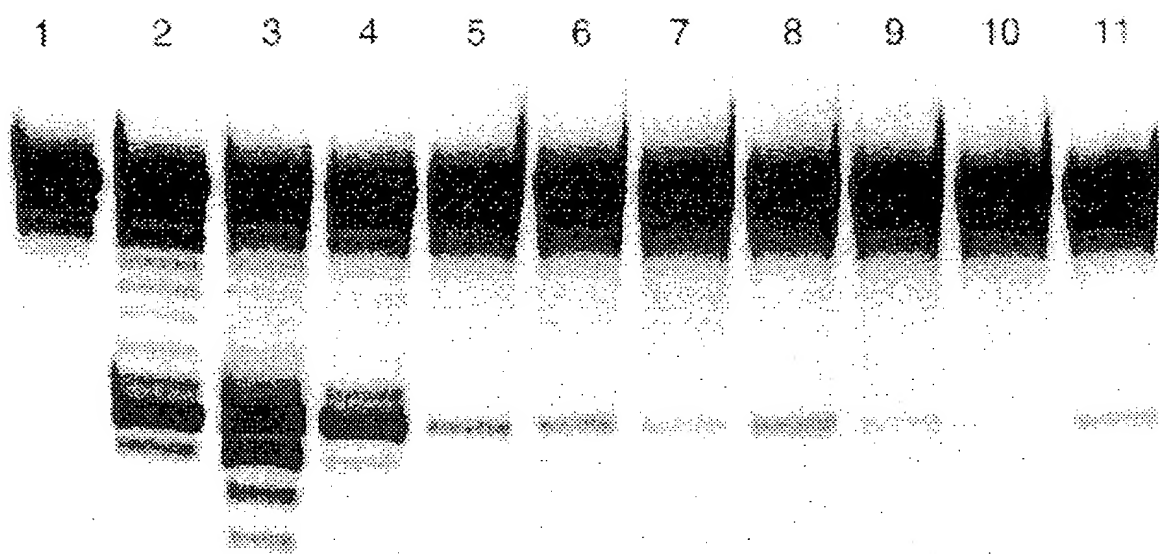


FIG. 34

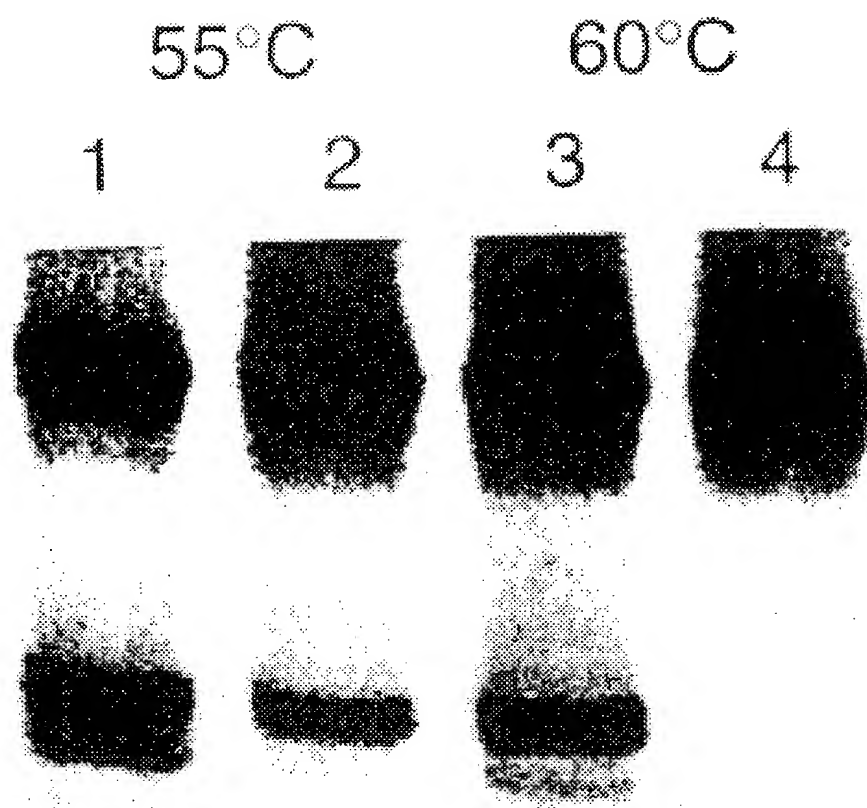


FIG. 35

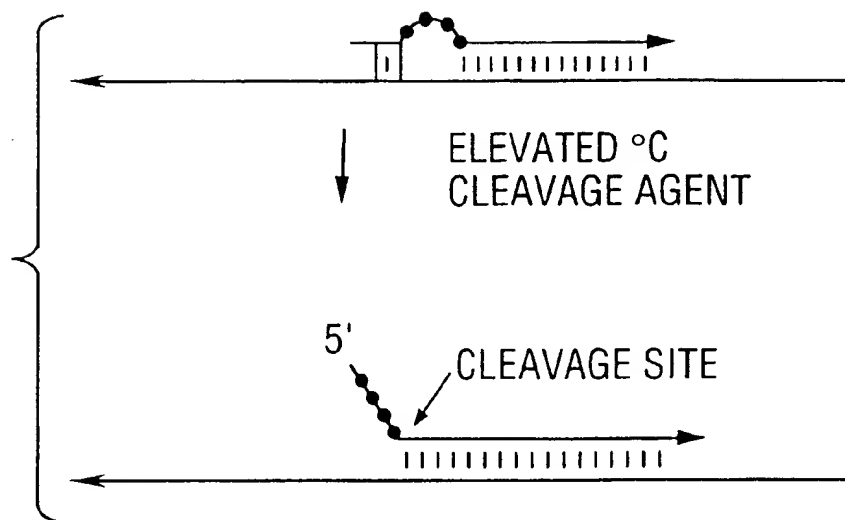


FIG. 36A

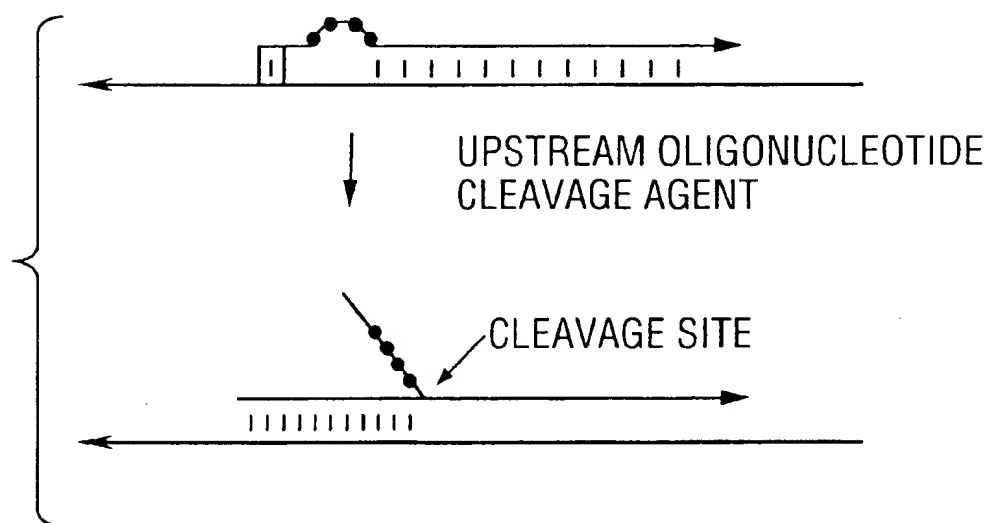


FIG. 36B

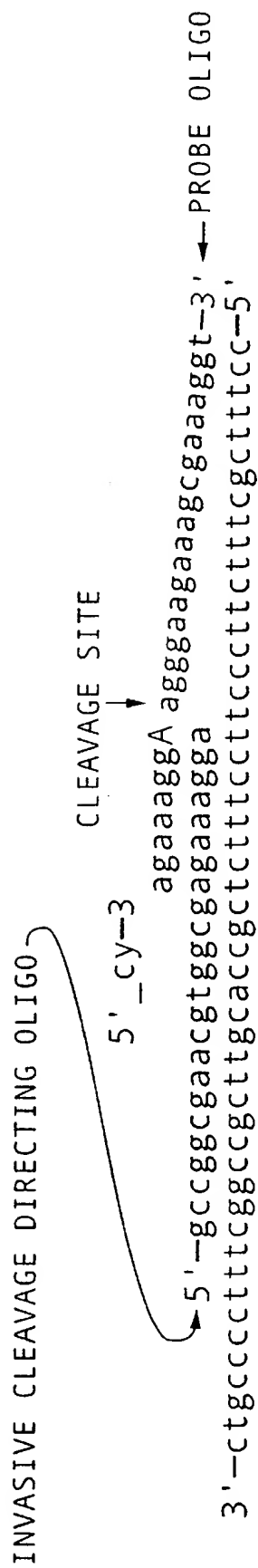


FIG. 37

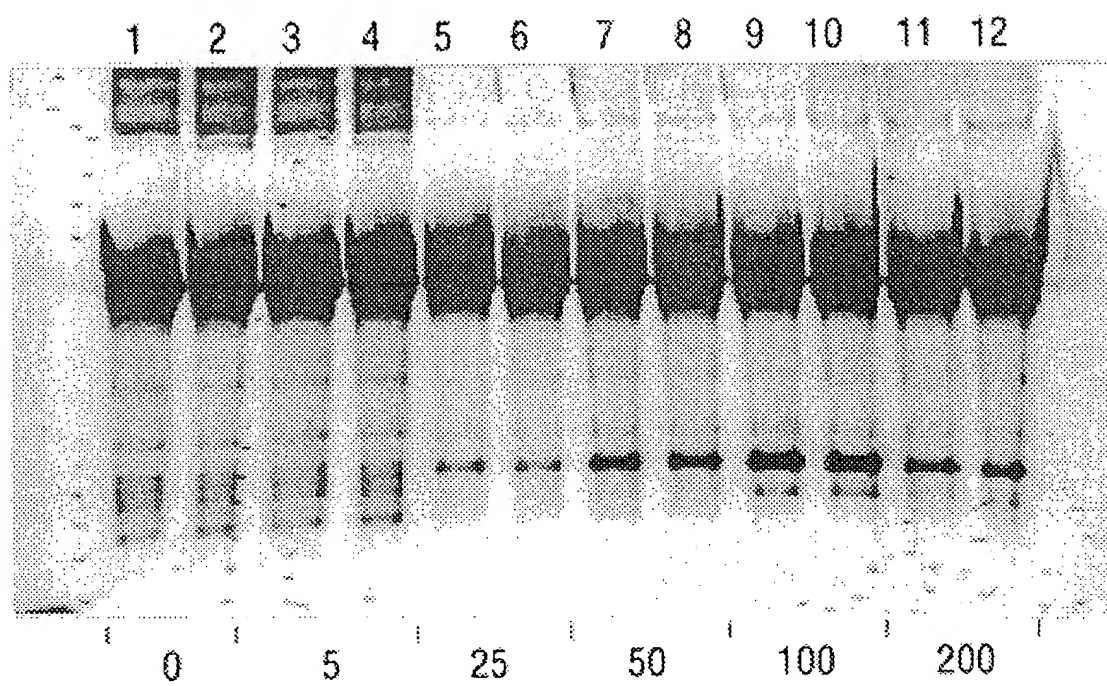


FIG. 38

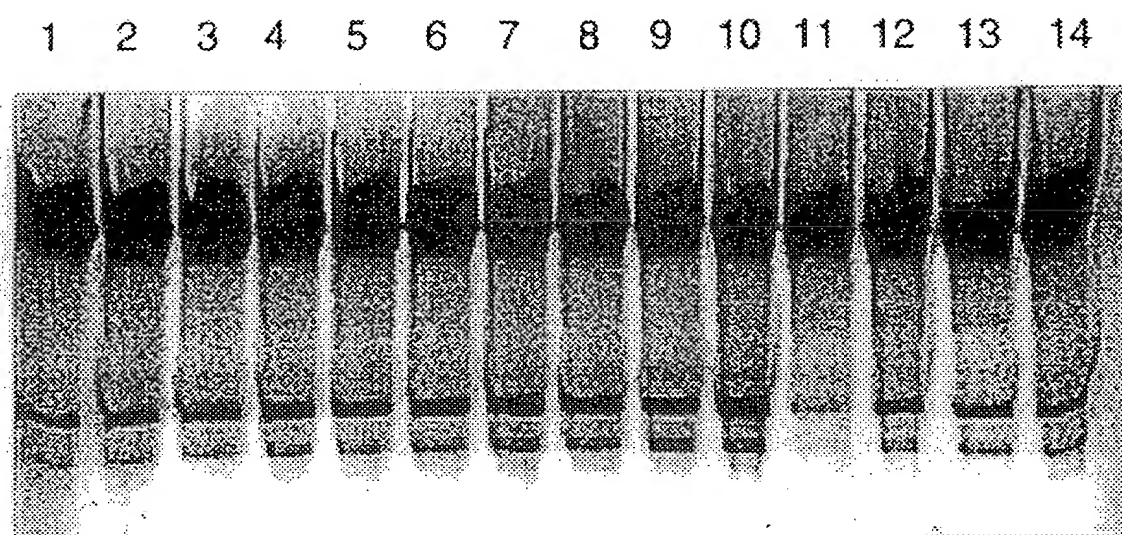


FIG. 39

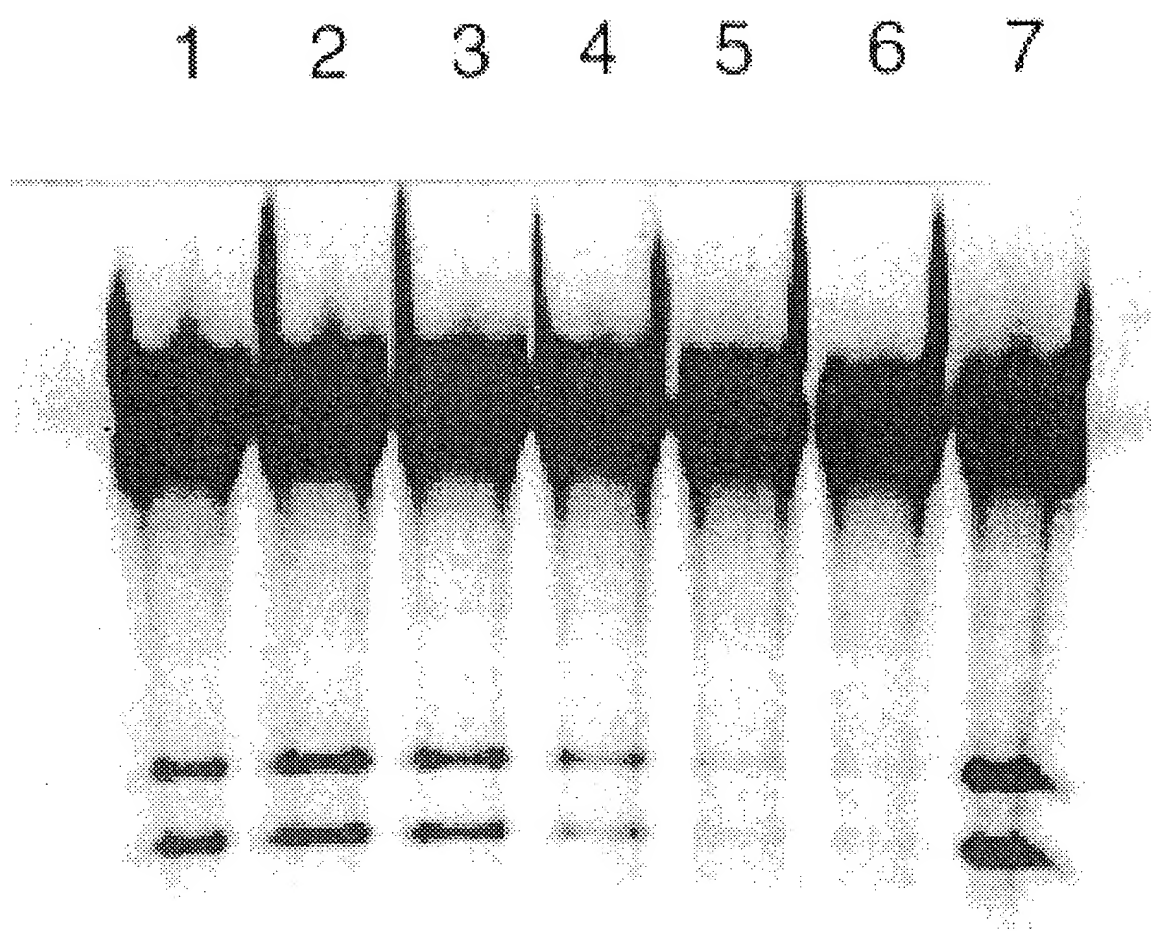


FIG. 40

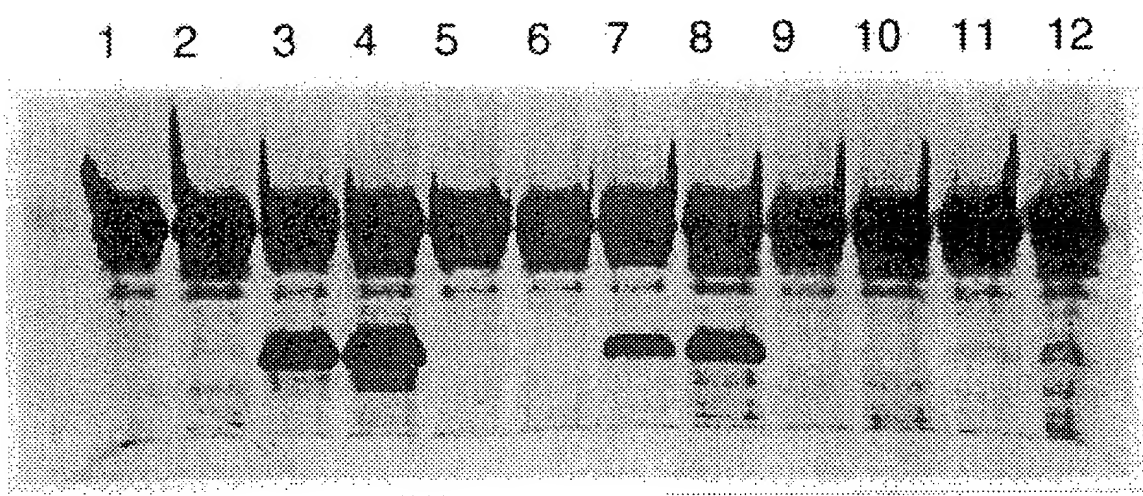
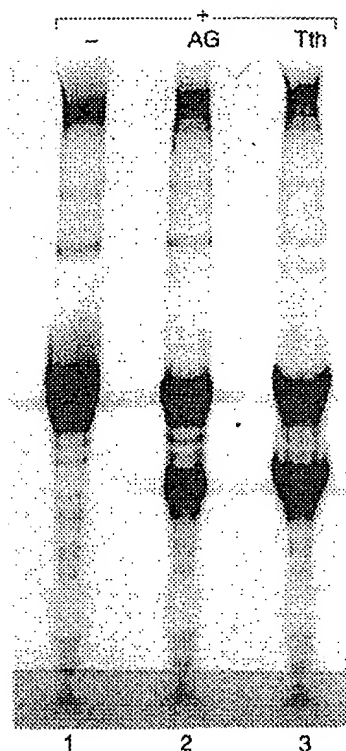
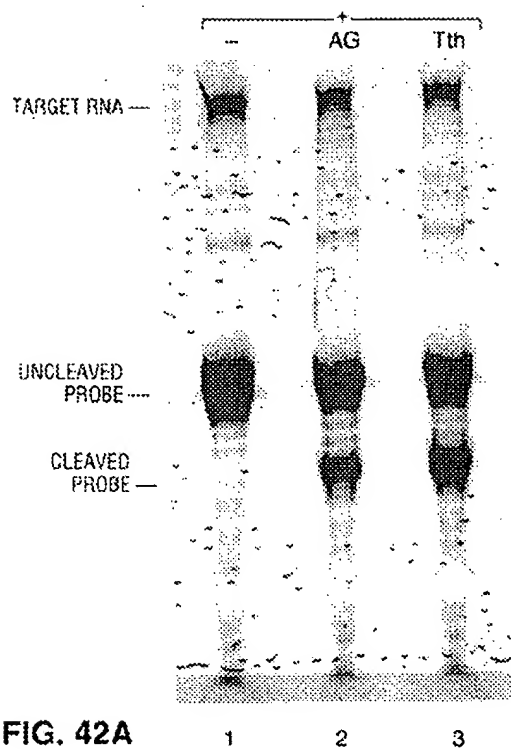


FIG. 41



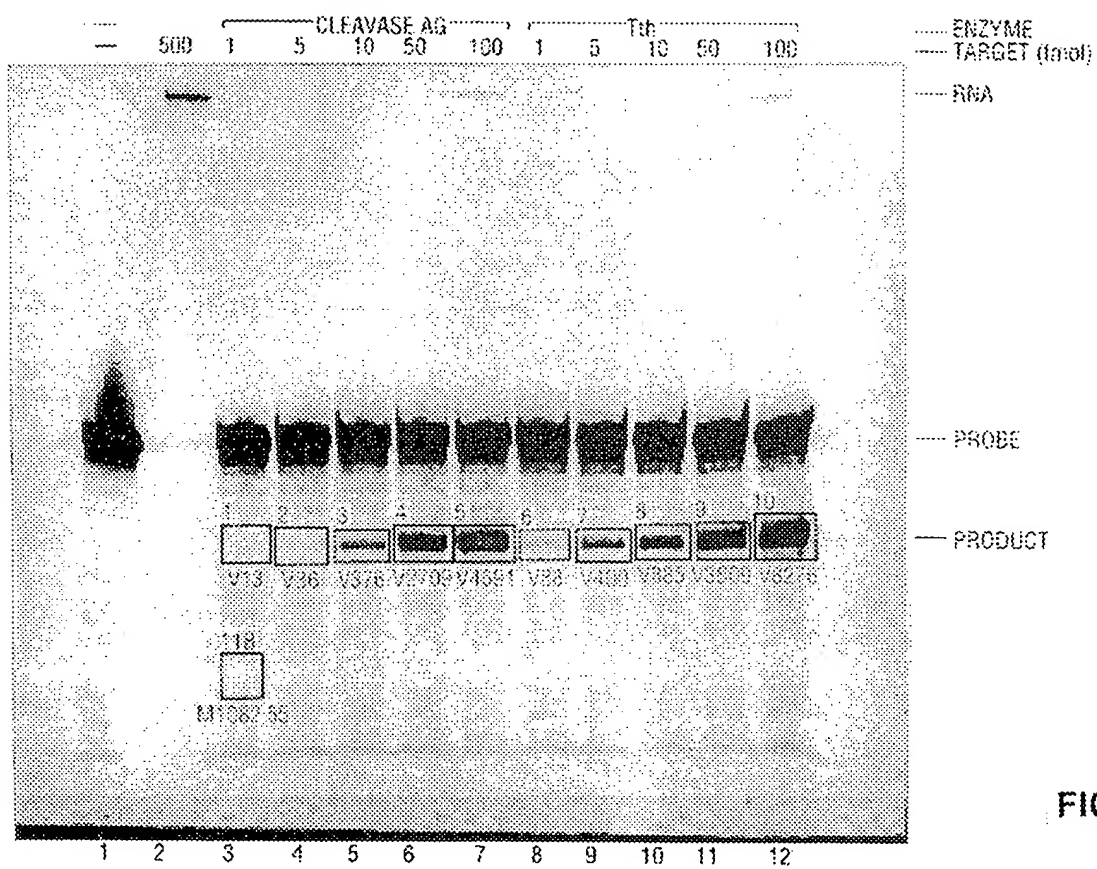


FIG. 43

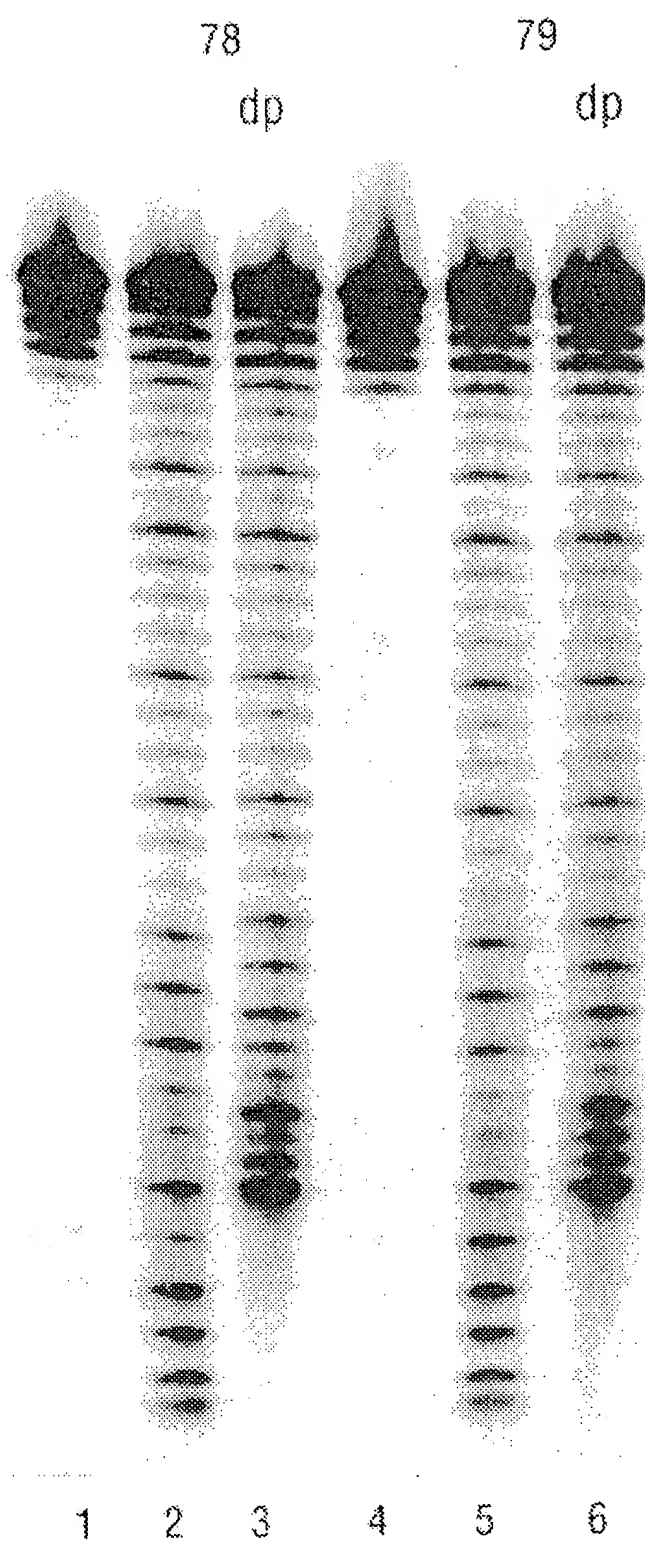


FIG. 44

70 (C10 amino T's)
74 (C6 amino T's)

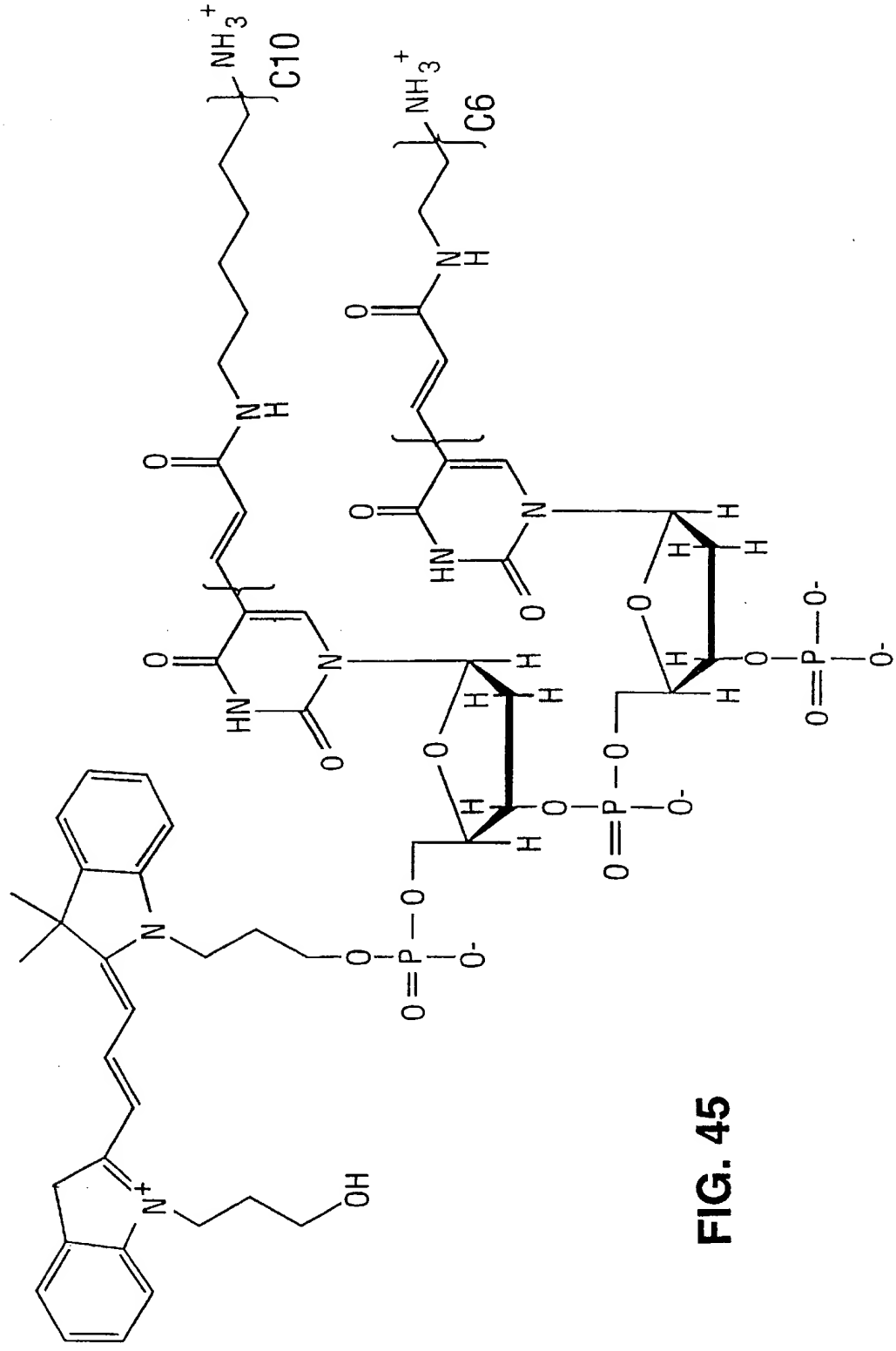


FIG. 45

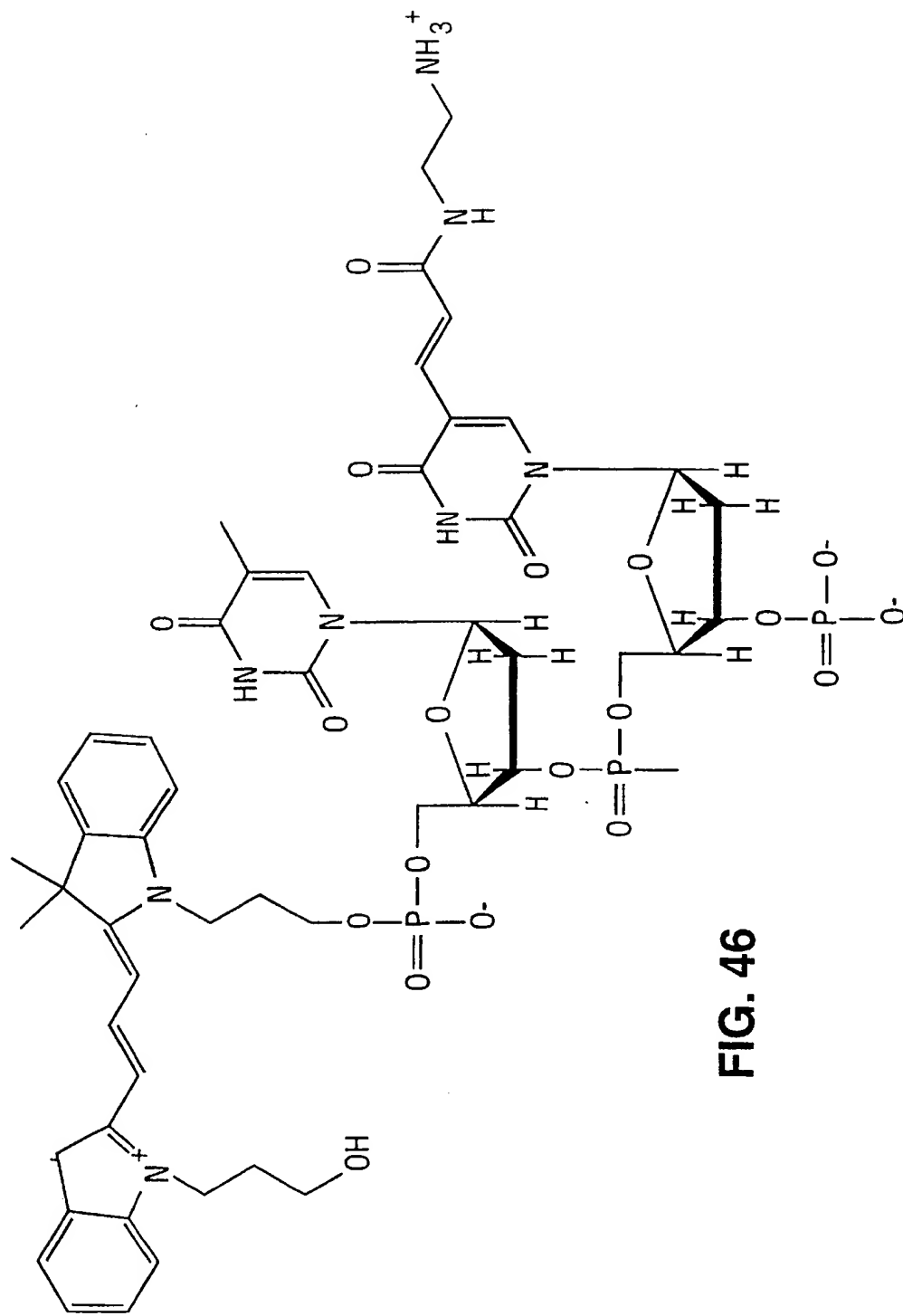
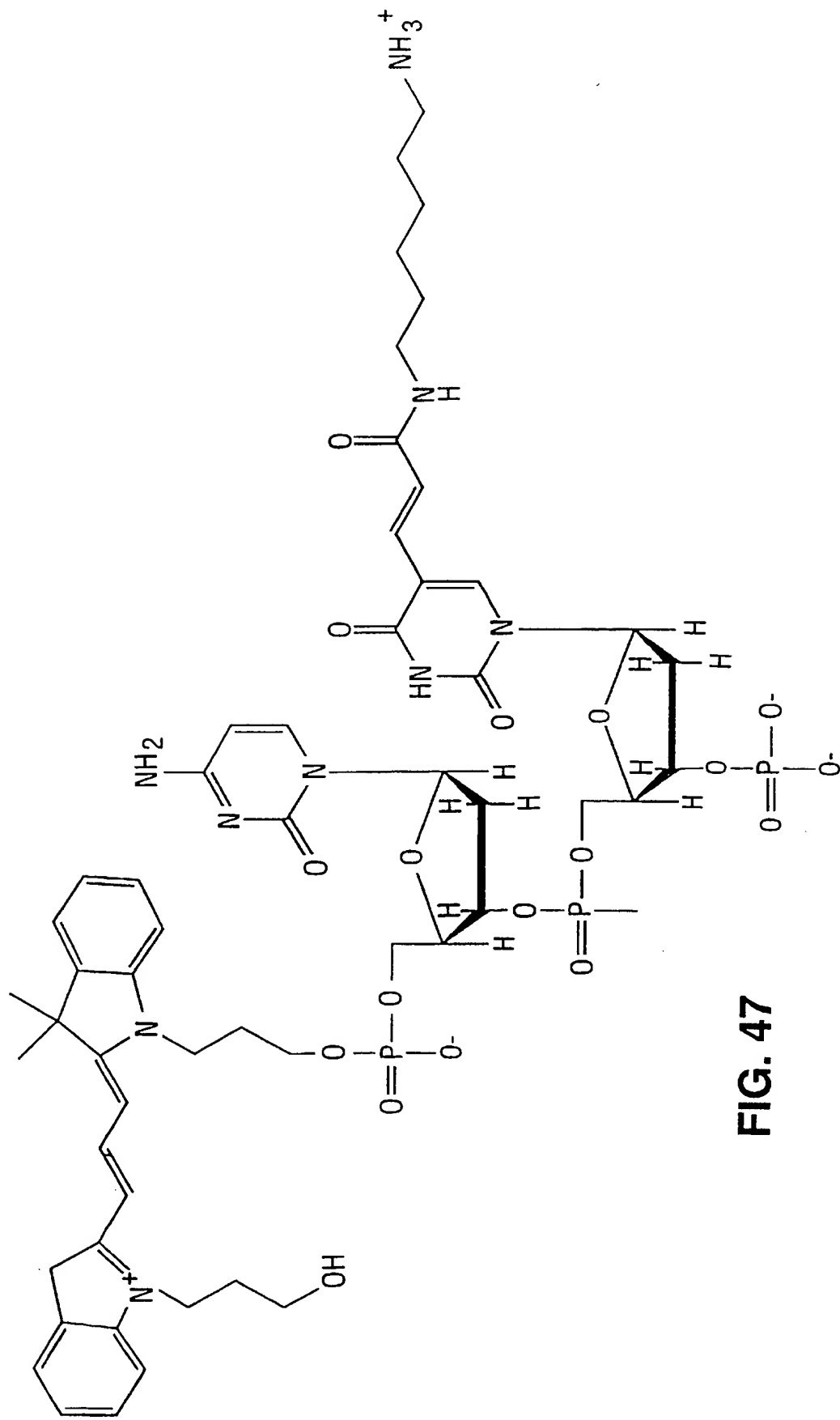


FIG. 46



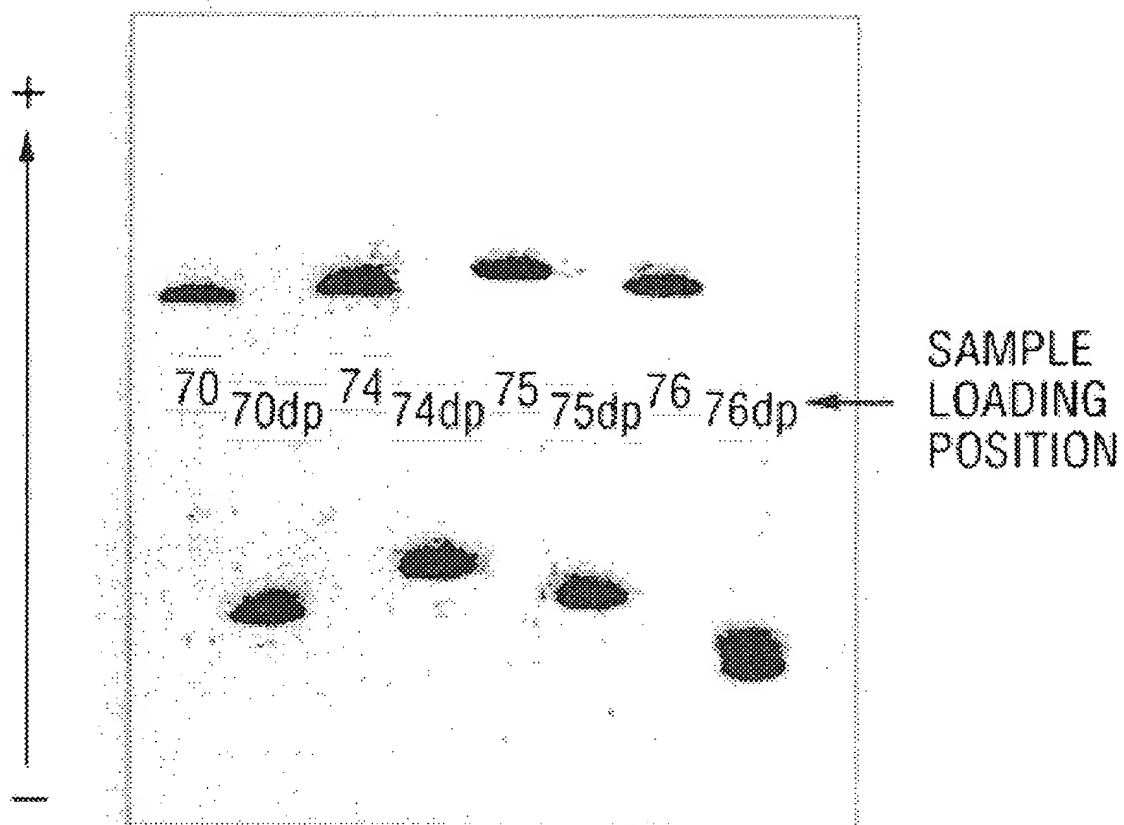


FIG. 48

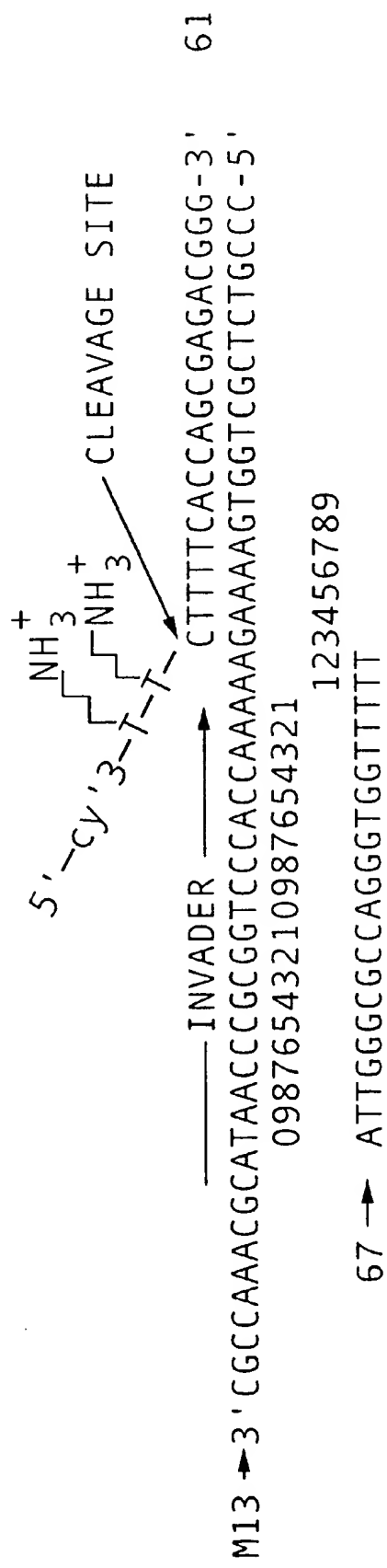


FIG. 49A

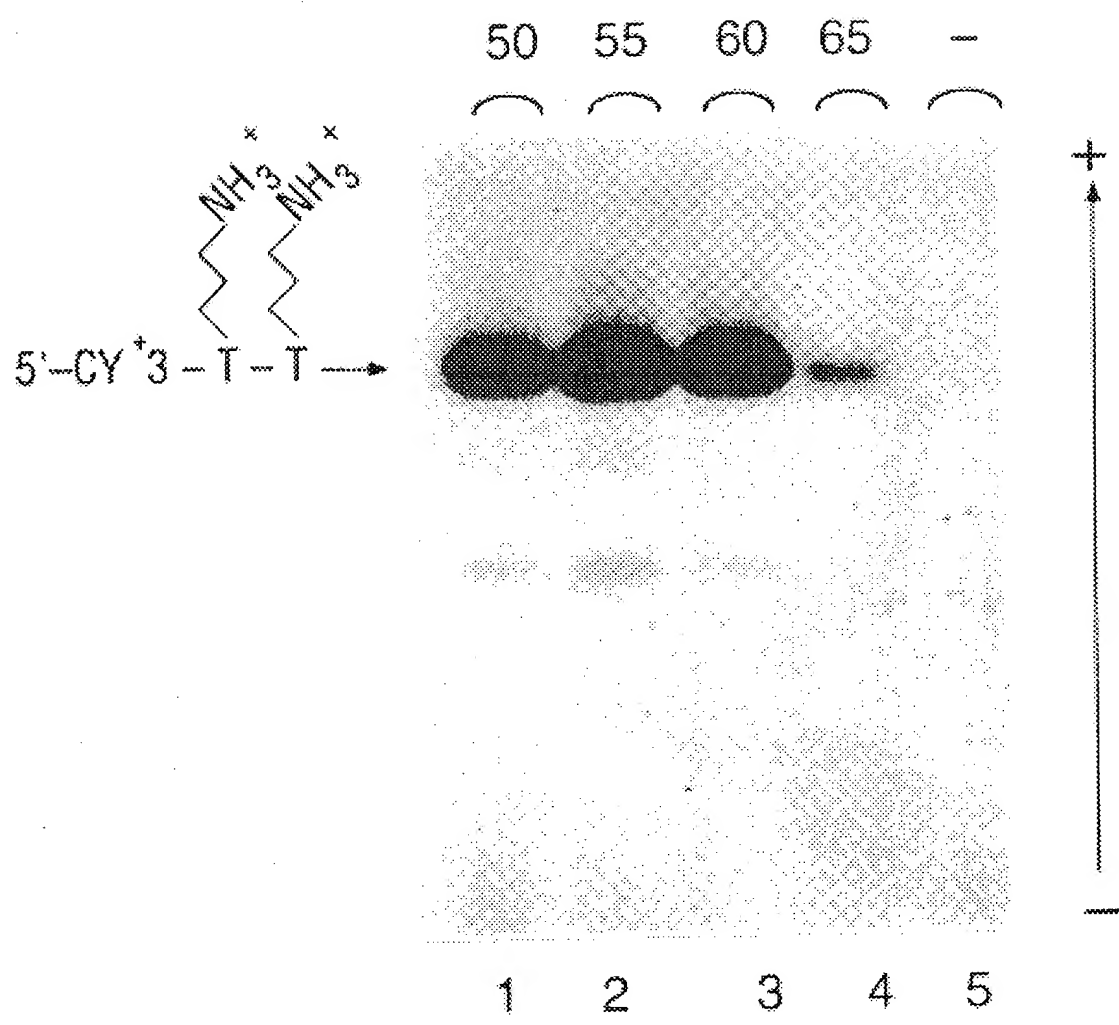


FIG. 49B

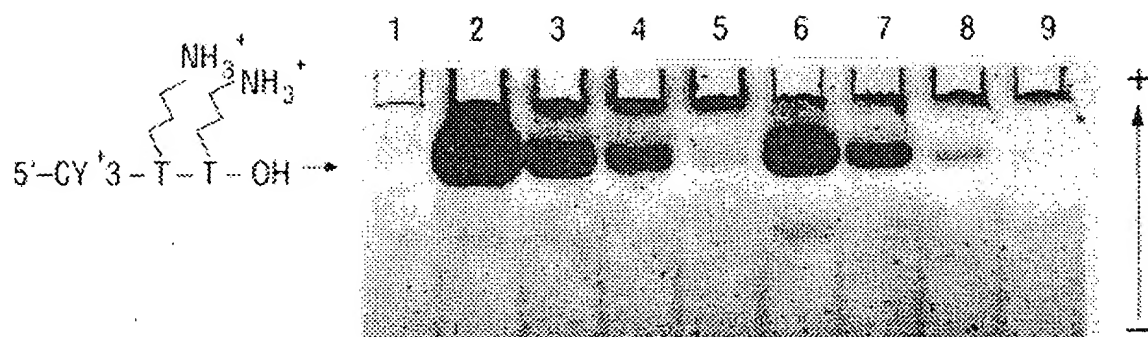


FIG. 50

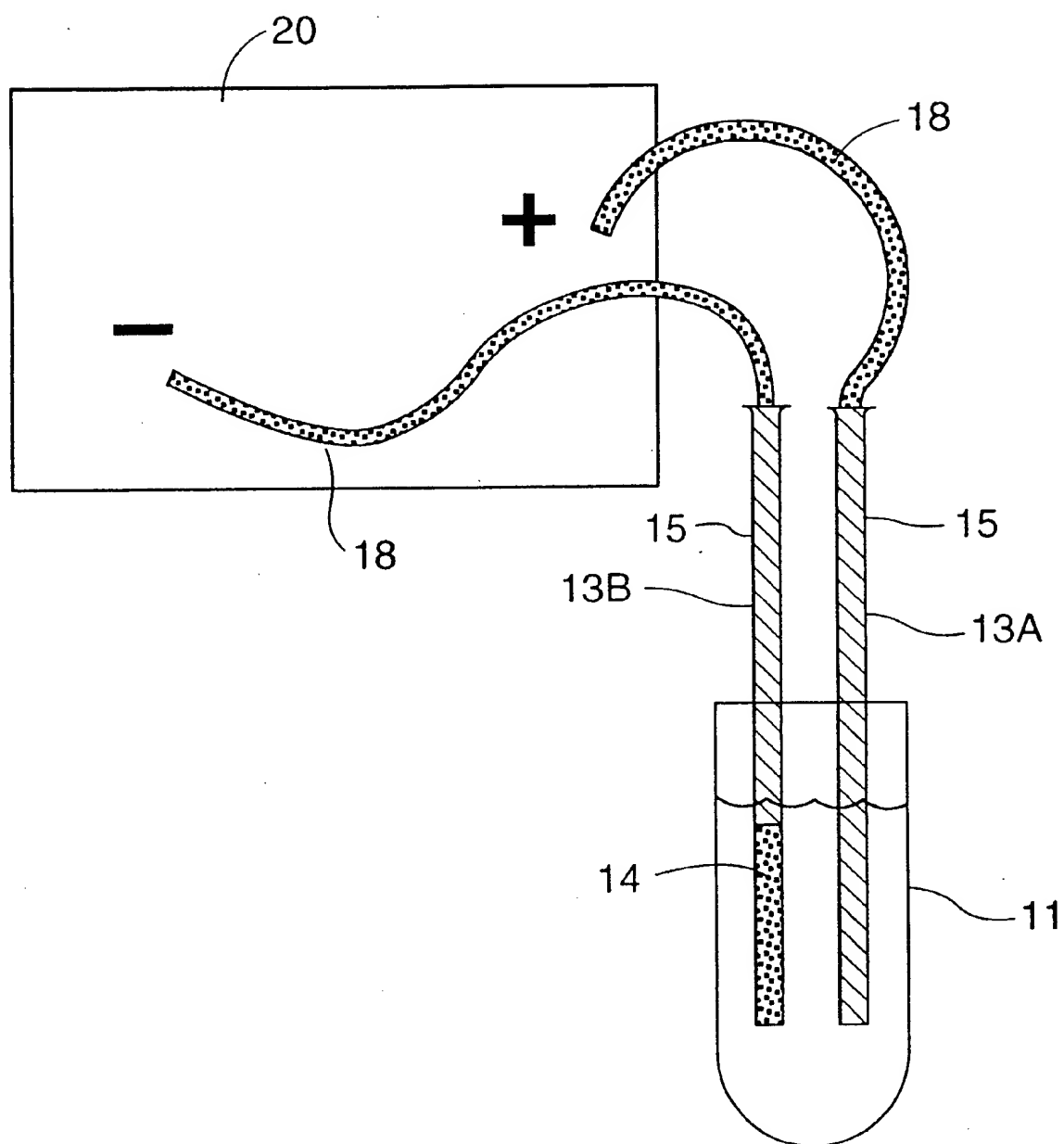


FIG. 51

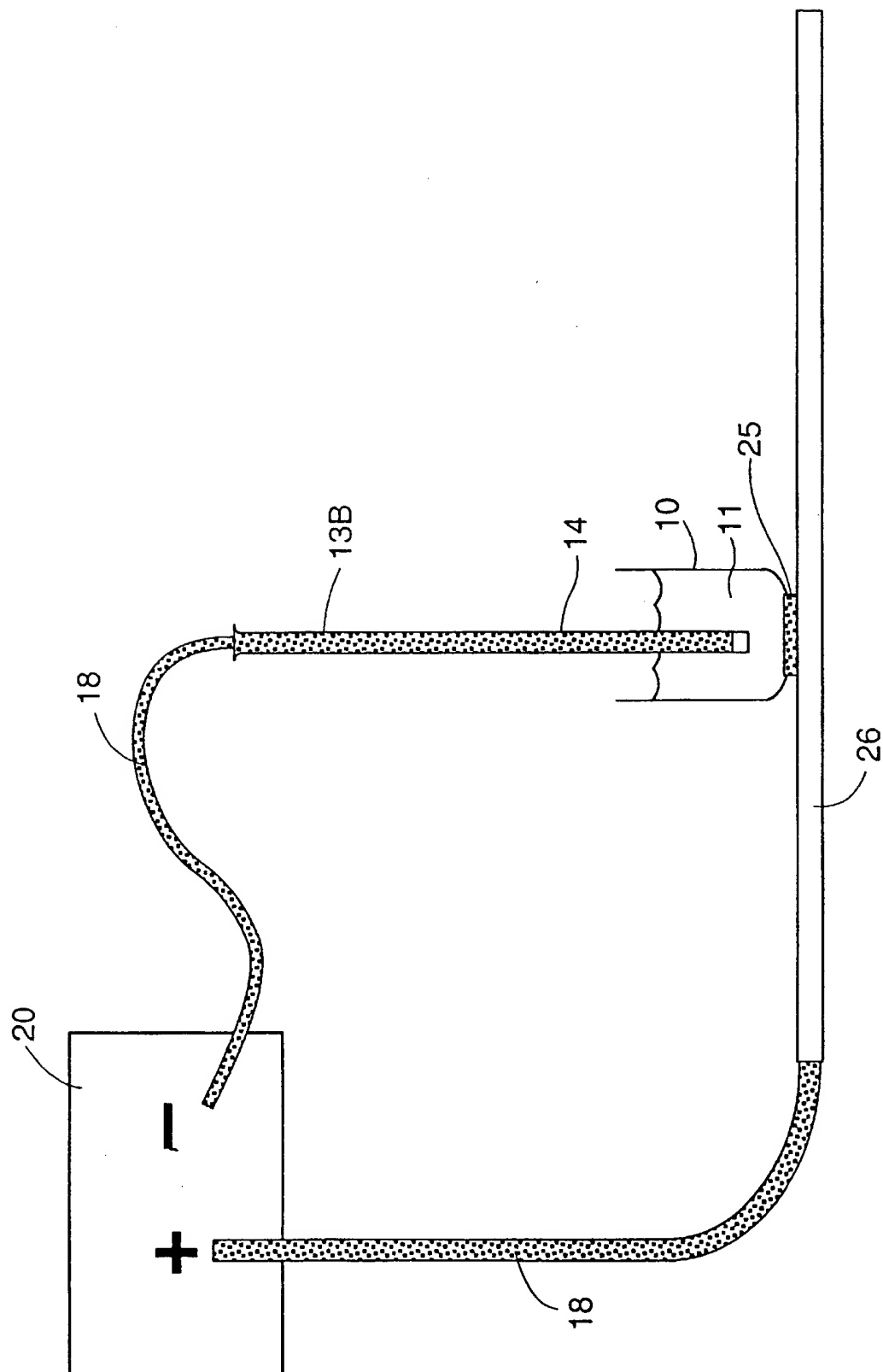


FIG. 52

PRIMER

- + C T A G

25 →

1 2 3 4 5 6

FIG. 53



FIG. 54A



FIG. 54B

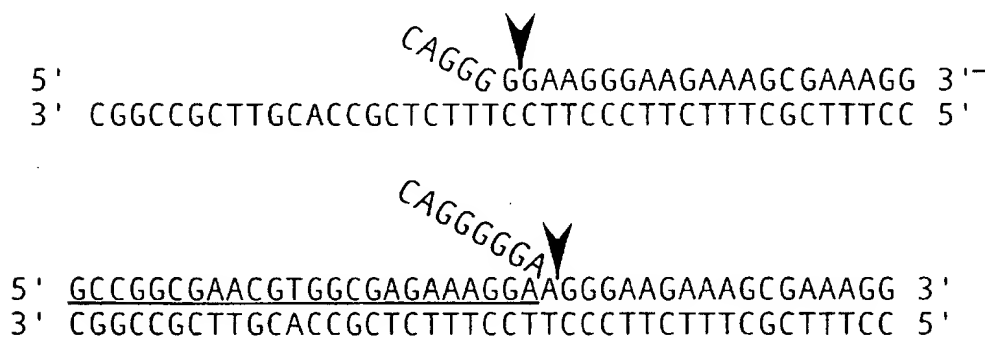


FIG. 54C



FIG. 54D

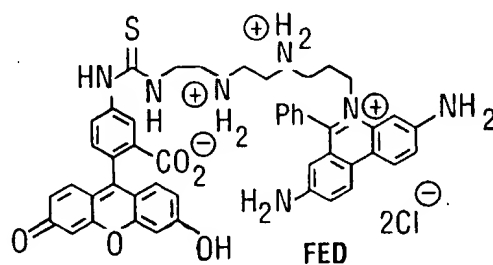
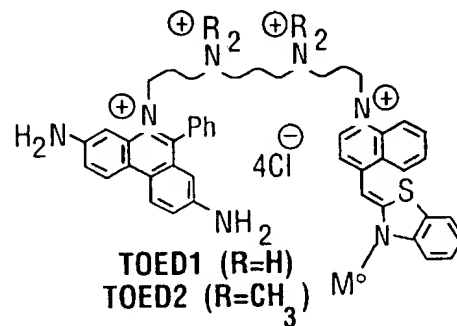
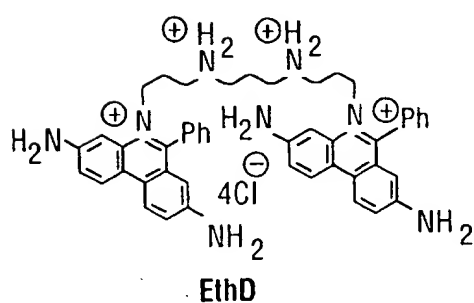
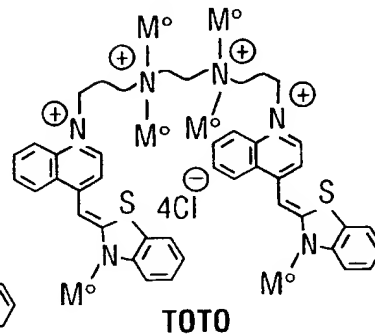
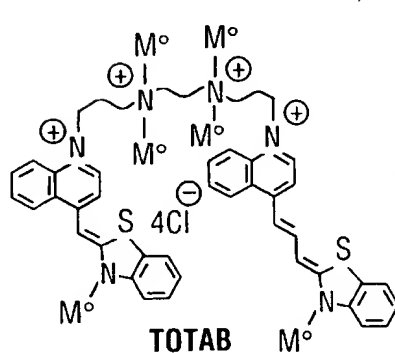
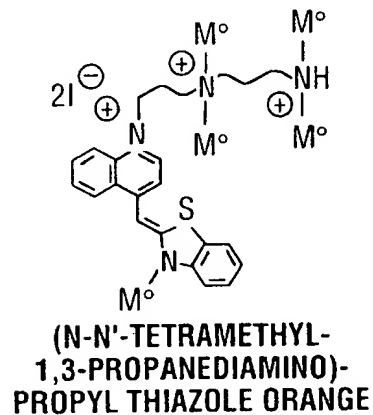
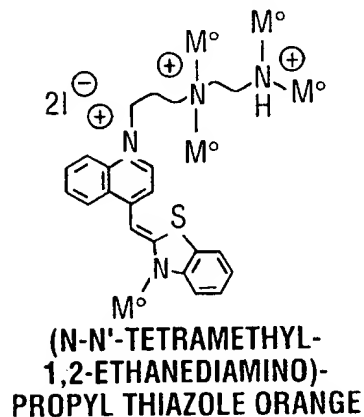
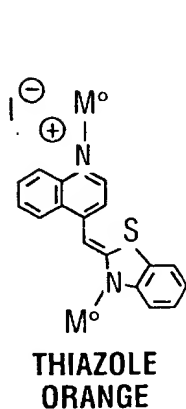
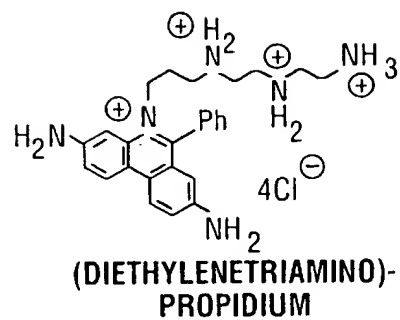
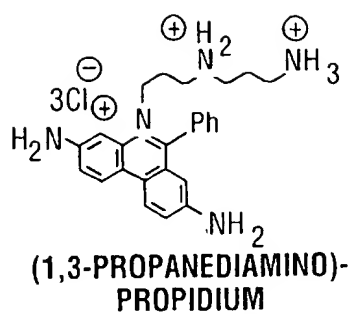
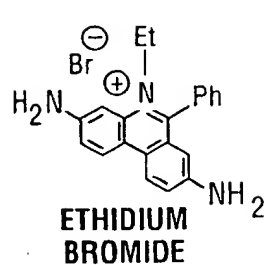
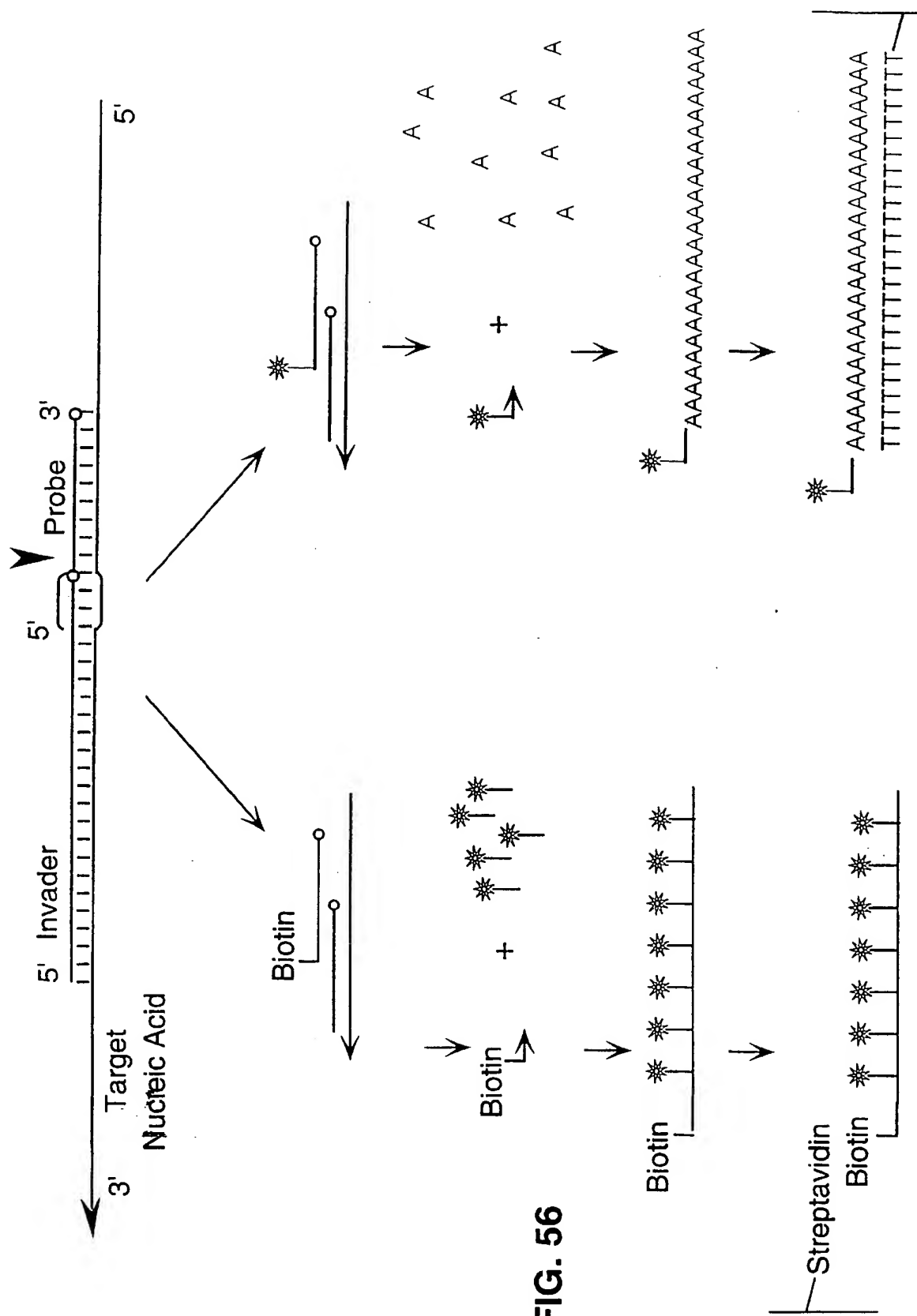


FIG. 55



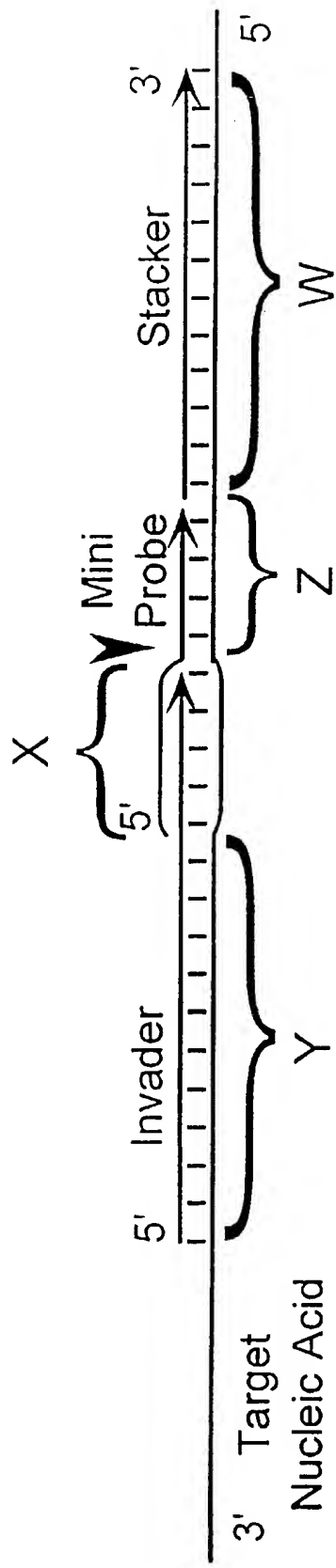


FIG. 57

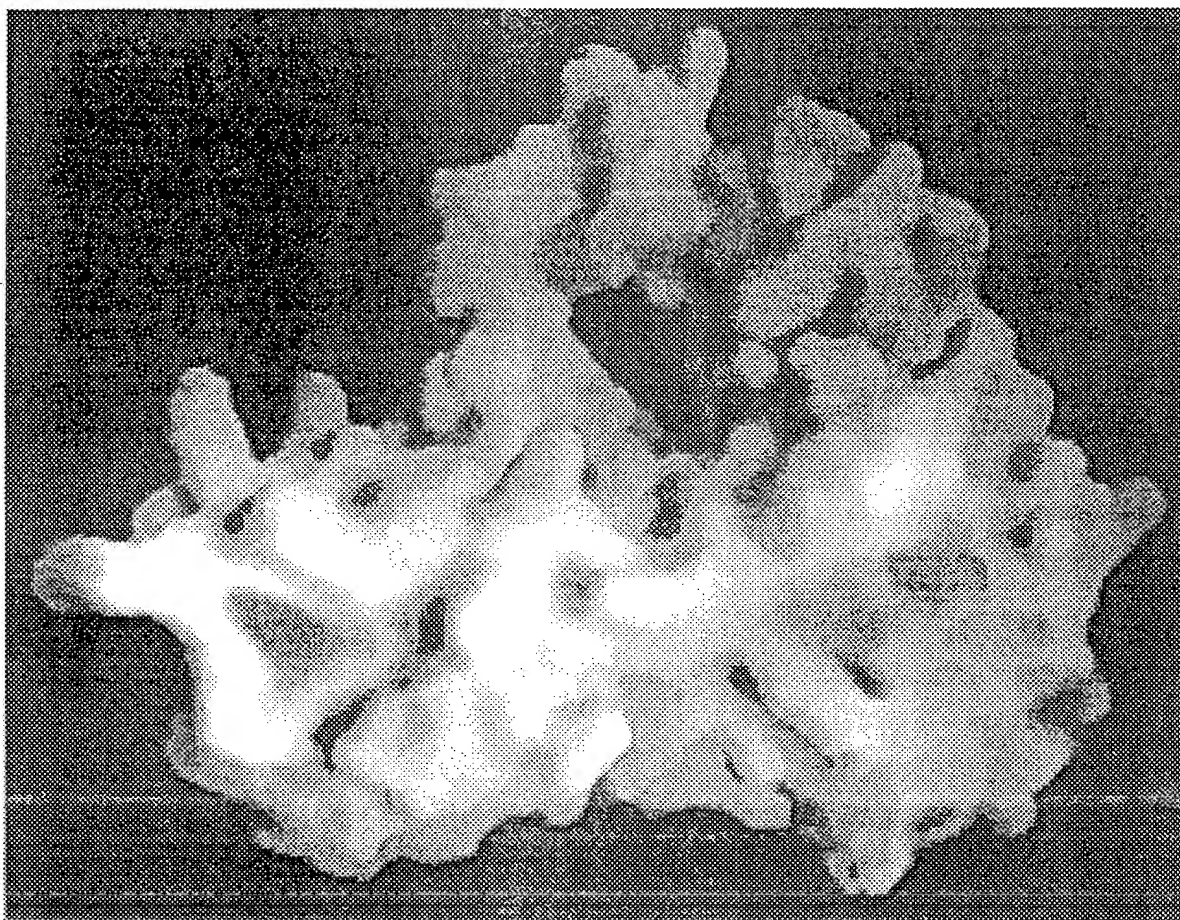


FIG. 58

	10	20	30	40	50	60	70
1	MGVQ-----	FGDEIPK--	NIISFEDL	KGKKVAID	GMNALYQF	LTSIRLRD	GSPLNRKGEITSAYNGV FY MJAFEN1.PRO
1	MGVP-----	IGETIPR--	KEIELENL	YGKKIAID	ALNAIYQF	LSTIRQKD	GTPLMDSKGRITSHLSGLFY PFUFEN1.PRO
1	MGIQGLAKLI	ADVAPSAI	RENDIKSY	FGRKVAID	ASMSIYQF	LIAVRQ--	GGDVLQNEEGETTSHLMGMFY HUMFEN1.PRO
1	MGIHGLAKLI	ADVAPSAI	RENDIKSY	FGRKVAID	ASMSIYQF	LIAVRQ--	GGDVLQNEEGETTSHLMGMFY MUSFEN1.PRO
1	MGIKGLNAII	SEHVPSAI	RKSDIKSF	FGRKVAID	ASMSLYQF	LIAVRQD	GGQLTNEAGETTSHLMGMFY YST510.PRO
1	MGVHSFWDIAG	-----	PTARPVRL	ESLEDKRM	AVDASIWIYQF	LKAVRDQ	EGNAVKN-----SHITGFFR YSTRAD2.PRO
1	MGVSGLWNILE	-----	PVKRPVKL	ETLVNKR	LAIIDASIIYQF	LKAVRDQ	KEGNQLKS-----SHVVGFFR SPORAD13.PRO
1	MGVQGLWKLE	-----	CSGROVS	PEALEGK	ILAVDISI	WLNQAL	KGVDRDHGNSIEN-----PHLLTLFH HUMXPG.PRO
1	MGVQGLWKLE	-----	CSGHRVS	PEALEGK	VLAVDISI	WLNQAL	KGVDRSHGNVIEN-----AHLTLFH MUSXPG.PRO
1	MGVQGLWKLE	-----	CSGRP	INPGTLEG	KILAVDISI	WLNQAV	KGARDRQGNAIQN-----AHLTLFH XENXPG.PRO
1	MTINGIWEWANHVV	-----	RKVPNET	MRDKT	L	SIDGHIW	YESLKGCEAHHQQT-----PNSYLVTFFT CELRAD2.PRO

	80	90	100	110	120	130	140					
64	KTIHLL	ENDITPIW	FDGGEPPK	LKEKTRK	VRRMKEK	AELKMKEAIKK	-----EDFEEAAKYAKRVSYLTP MJAFEN1.PRO					
64	RTINL	MEAGIKPV	YVFDGEP	PEFKKKE	LKRREAR	EEAEKWR	EALKEK-----GEIEEARKYAQRATRVNE PFUFEN1.PRO					
70	RTIRM	MENGIKPV	YVFDGK	PPQLKSG	ELAKRS	ERRAEAEK	QLQQAQAA-----GAEOEVEKFTKRLVKVTK HUMFEN1.PRO					
69	RTIRM	-ENG	IKPVYV	FDGKPP	QLKSG	ELAKRS	ERRAEAEKQLQQAQEA-----GMEEVEKFTKRLVKVTK MUSFEN1.PRO					
71	RTL	MIDNGIK	PCYVFD	GKPPDL	KSHEL	TKRSSRR	VETEKKLA-----TTELEKMKQERRLVKVS YST510.PRO					
61	RICKLL	YFGIRPV	FVFDGG	VPVLKRE	TIRQK	ERRQKRES	AKSTARKLLALQLQNGSNDNKRDSDEVTM YSTRAD2.PRO					
61	RICKLL	FFGIKPV	FVFDGG	APSLKR	QTIQK	RQARRLD	REENATVTANKLLALQMRHQAMLKRDAD	EVTDQ SPORAD13.PRO				
61	RLCKLL	FFRIRPI	FVFDGD	APLLKK	QTLV	KRRQRKDL	ASSDSRKTT	EKLKTF	LKRQAIKTERIAATVTG HUMXPG.PRO			
61	RLCKLL	FFRIRPI	FVFDGD	APLLKK	QTLAK	RRQRKDS	ASIDS	RKTT	EKLKTF	LKRQAL	KTDRIAASVTG MUSXPG.PRO	
61	RLCKLL	FFRIRPI	FVFDGE	APLLKR	QTLAK	RRQR	QTDK	ASND	ARKT	NEKLLR	TFLKRQAIKAERIAATVTG XENXPG.PRO	
60	RIQRLL	LELKII	PIVVD	INASSA	HESKDQ	NEFV	PRKRRS	FGDSPFTNLV	-----			CELRAD2.PRO

FIG. 59A

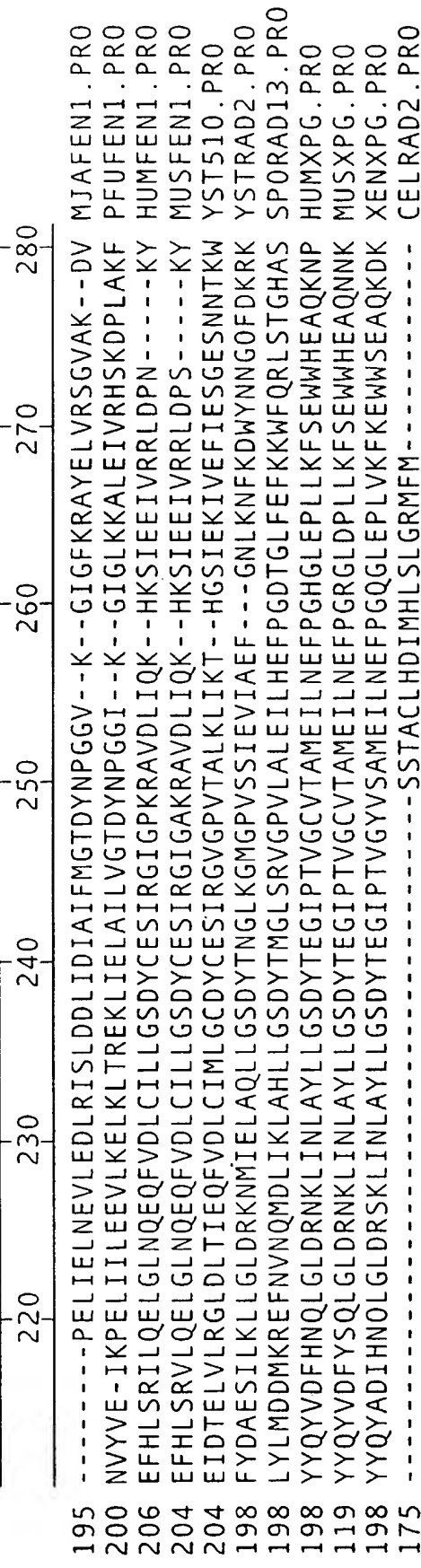
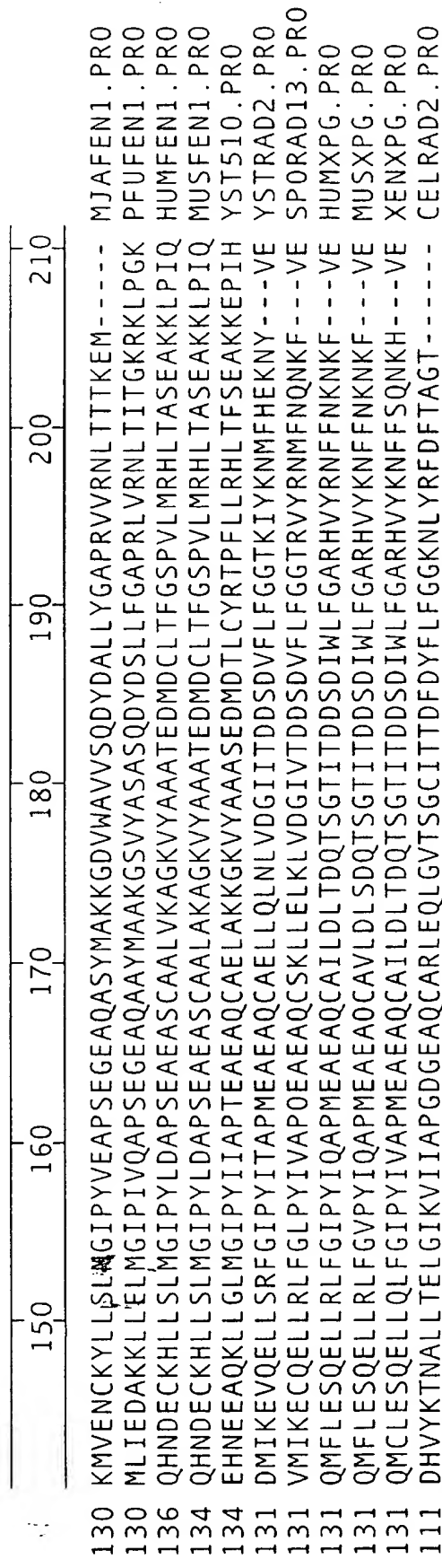


FIG. 59B

	290	300	310	320	330	340	350
251	LKKEVEYYDEIKKIFKEPKV-----	TD--	NYSLSLKL	PDKEGI	IKFLVD	ENDFN	YD MJAFEN1.PRO
265	QKQSDVDLYAIKEFFLNPPV-----	TD--	NYNLVWRD	PDDEEG	ILKFLC	DEHDF	SEE PFUFEN1.PRO
269	PVPENWLHKEAHQLFLEPEV-----	LDPE	SVELKWSE	PNEEEE	LIKFMCG	EKFSEE	HUMFEN1.PRO
267	PVPENWLHKEAQQLFLEPEV-----	VDPE	SVELKWSE	PNEEEE	LVKFMC	GKQFSEE	MUSFEN1.PRO
272	KIPEDWPYKQARMLFLDPEV-----	IDGNE	INLKWSP	PKKEKE	LIEYLC	DDKKF	SEE YST510.PRO
265	QETENKFEKDLRKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVDPDLMLRSFMKTQLGWPHE	YSTRAD2	2.PRO				
268	KNDVNTPVKKRINKLVGK-IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGI	PDLD	DEL	QFLM	ATV	GWSKQ	SPORAD13.PRO
268	KIRPNPHDTKVKKKL--RTLQLTPGFPNPAVAEAYLKPVVDDSKGSFLWGK	PDLD	KIRE	FCQRY	FGWNRT		HUMXPG.PRO
268	KVAENPYDTKVKKKL--RKLQLTPGFPNPAVADAYLRPVVDDSRGSFLWGK	PDVD	KIRE	FCORY	FGWNRM		MUSXPG.PRO
268	KMRPNPNDTKVKKKL--RLLDLQQSFNPAVASAYLKPVVDESKSAFSWGR	PDLE	QIRE	FCESR	FGWYRL		XENXPG.PRO
194	-----EKKVSRPHLISTAILLGCDYFORGVQNI	GIVSV	FD-IL	GEFG	DDGNEE	IDPHVIL	DRFASYVRE CELRAD2.PRO

	360	370	380	390	400	410	420
300	RVKKHVDKLYNLIA-----						MJAFEN1.PRO
314	RVKNGLERLKKAI-----						PFUFEN1.PRO
320	RIRSGVKRLSKSRQGS-TQGRLD	DDFFKVT					HUMFEN1.PRO
318	RIRSGVKRLSKSRQGS-TQGRLD	DDFFKVT					MUSFEN1.PRO
323	RVKSGISRLKKGLKSG-IQGRLD	GFFOVV					YST510.PRO
335	KSDEILIP	IRDVNKRKK					KGKQ YSTRAD2.PRO
337	RTNEVLLP	VIQDMHKKOF					SPORAD13.PRO
336	KTDESLFPVLKQLDAQQTQLRID	SFFRLAQ	QEKEDAKRIKSQRL	NRAVTCMLRKEKE	AAASEI	EAVSVAM	HUMXPG.PRO
336	KTDESLYPVLKHLNAHQTLRID	SFFRLAQ	QEKQDAKLKSHRL	SRAVTCMLRKEERE	EKAPELT	TKVTEAM	MUSXPG.PRO
336	KTDEVLLPVLKQLNAQQTQLRID	SFFRLAQ	HEAAG--LKSQRL	RRAVTCMKR	KERDVE	AEVEAAVAM	XENXPG.PRO
257	EIPARSED	TQRKLRLRRKKYNFPVGF	PNCD	AVHNAITMYLRPPV	SSEIPKII	PR-----	AANFQQVAEIM CELRAD2.PRO

FIG. 59C

	430	440	450	460	470	480	490
314	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
348	-----	-----	-----	-----	-----	-----GSL	HUMFEN1.PRO
346	-----	-----	-----	-----	-----	-----GSL	MUSFEN1.PRO
351	-----	-----	-----	-----	-----	-----PK-T	YST510.PRO
357	KRINEFF	-----	-----	-----	-----	-----	YSTRAD2.PRO
359	SNLTQFFEGGNTNVYAPRVAYHFKSKRLENALSSFKNQISNQSPMSEEEIQADADAFGESKGSDELOSRIL	-----	-----	-----	-----	-----	SPORAD13.PRO
406	EKEFELDKAKRKTQKRGITNTLEESSLKRRLSDSKRNTCGGFLGETCLSESSDGSSEHAESSLM	-----	-----	-----	-----	-----	HUMXPG.PRO
406	EKEFELDDAKGKTOKREL PYK	-----	-----KETSVPKRRRPSGNGGFLGDPYCSESPQESSCEDGEGSSVM	-----	-----	-----	MUSXPG.PRO
403	ERECTNQKRGQKTNKTS	-----	-----QGTKRKPTCESQEDQDPGGGFIGIELKTLSSKAYSSD	-----	-----	-----	XENXPG.PRO
322	MKECGWPATRTQKELALSIRRKVHLTTTVAQTRIPDFFAATKSKNFTPIVEPCESLEDYISANN	-----	-----	-----	-----	-----T	CELRAD2.PRO

	500	510	520	530	540	550	560
314	-----	-----	-----	-----	-----	-----	NKTKQKTL MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	KSGKQSTL PFUFEN1.PRO
352	SAKRKEPEPKGST	-----	-----	-----	-----	-----	KKKAKTGAAG HUMFEN1.PRO
350	SAKRKEPEPKGPA	-----	-----	-----	-----	-----	KKKAKTGGAG MUSFEN1.PRO
354	KEQLAAAKRAQE	-----	-----	-----	-----	-----	NKKLNKNKNK YST510.PRO
364	-----	-----	-----PREYISGDKKLNTSKRISTATGKL	-----	-----	-----	YSTRAD2.PRO
429	RRKKMMASKNSSDSDSDSEDNFLASLTPKTNSSSISIENLPRKTKLSTSL	-----	-----	-----	-----	-----	SPORAD13.PRO
476	NVQRRTAAKEPKTSASDSONSVKEAPVKNGGATTSSSDSDDDGGKEKMLVLTARSVFGKKRRKLRARG	-----	-----	-----	-----	-----	HUMXPG.PRO
469	SARQSAEESKIGCSDVPLVRDSPHGRQGCVSTSSDSEDGEDKAKTVLVTARPVFGKKRRKLSMK	-----	-----	-----	-----	-----	MUSXPG.PRO
458	-----GSSSDAEDLPSGLIDKQSQSGIVGROKASNKVESSSDDEDRTVMVTAKPVFGKKTSKTMKE	-----	-----	-----	-----	-----	XENXPG.PRO
387	WMRKRKRSESPQILQHHAKRQVPDRK	-----	-----	-----	-----	-----	RSVKIRAFKPYPTDVI CELRAD2.PRO

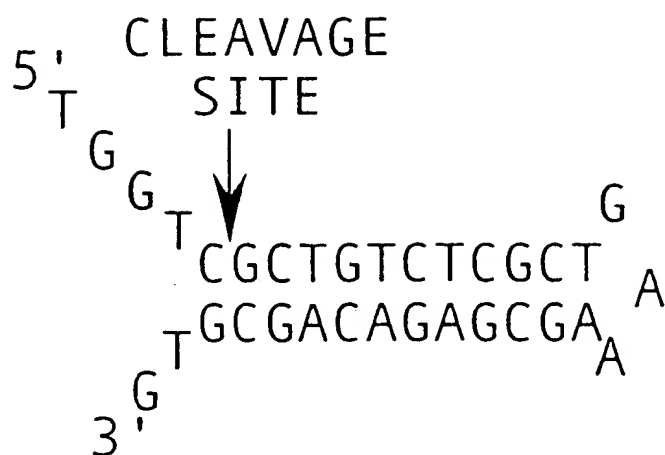
FIG. 59D

322 DAWFKZ
335 ESWFKR
375 KFKRGK
373 KFRRGK
377 VTKGRR
390 ---RKM
483 SKRRRK
546 RKRKTZ
538 RRKKKT
523 TVKRK
429 ELGDSD

MJAFEN1.PRO
PFUFEN1.PRO
HUMFEN1.PRO
MUSFEN1.PRO
YST510.PRO
YSTRAD2.PRO
SPORAD13.PRO
HUMXPG.PRO
MUSXPG.PRO
XENXPG.PRO
CELRAD2.PRO

FIG. 59E

S-33



11-8-0

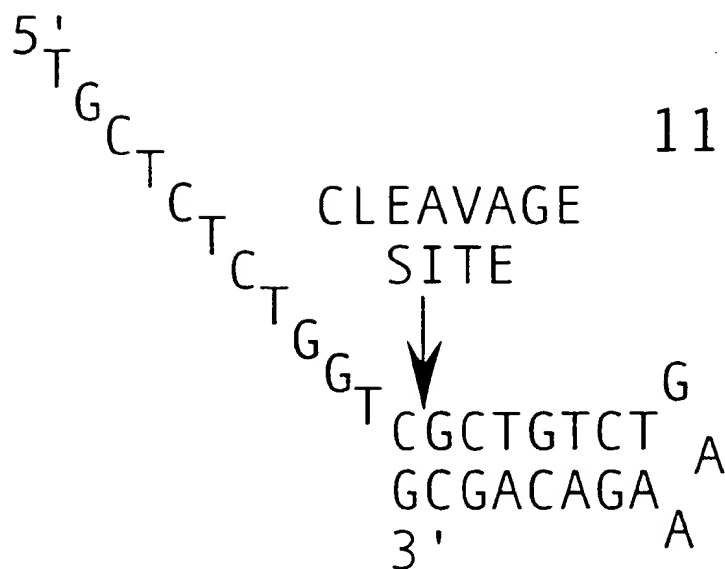


FIG. 60

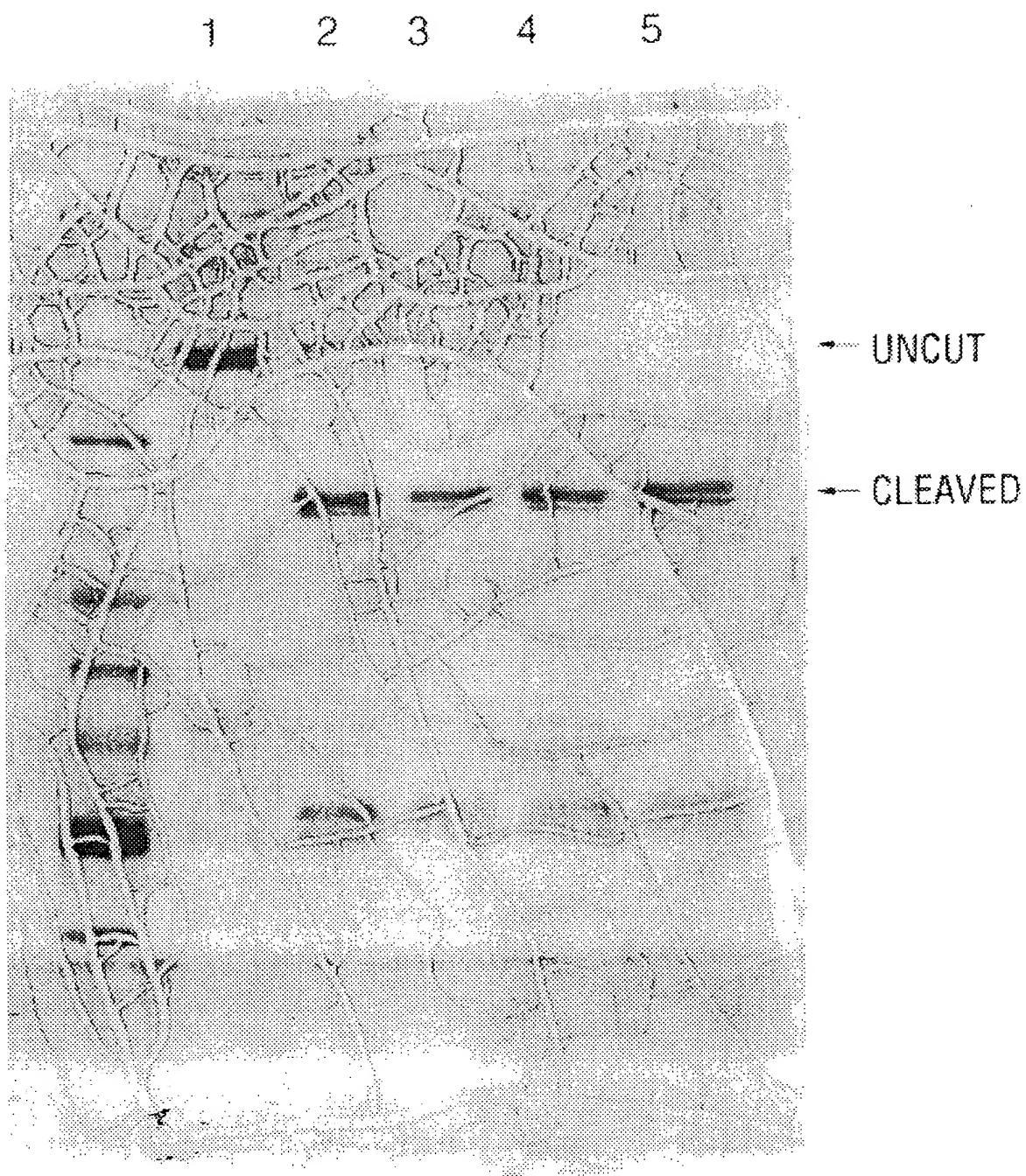


FIG. 61

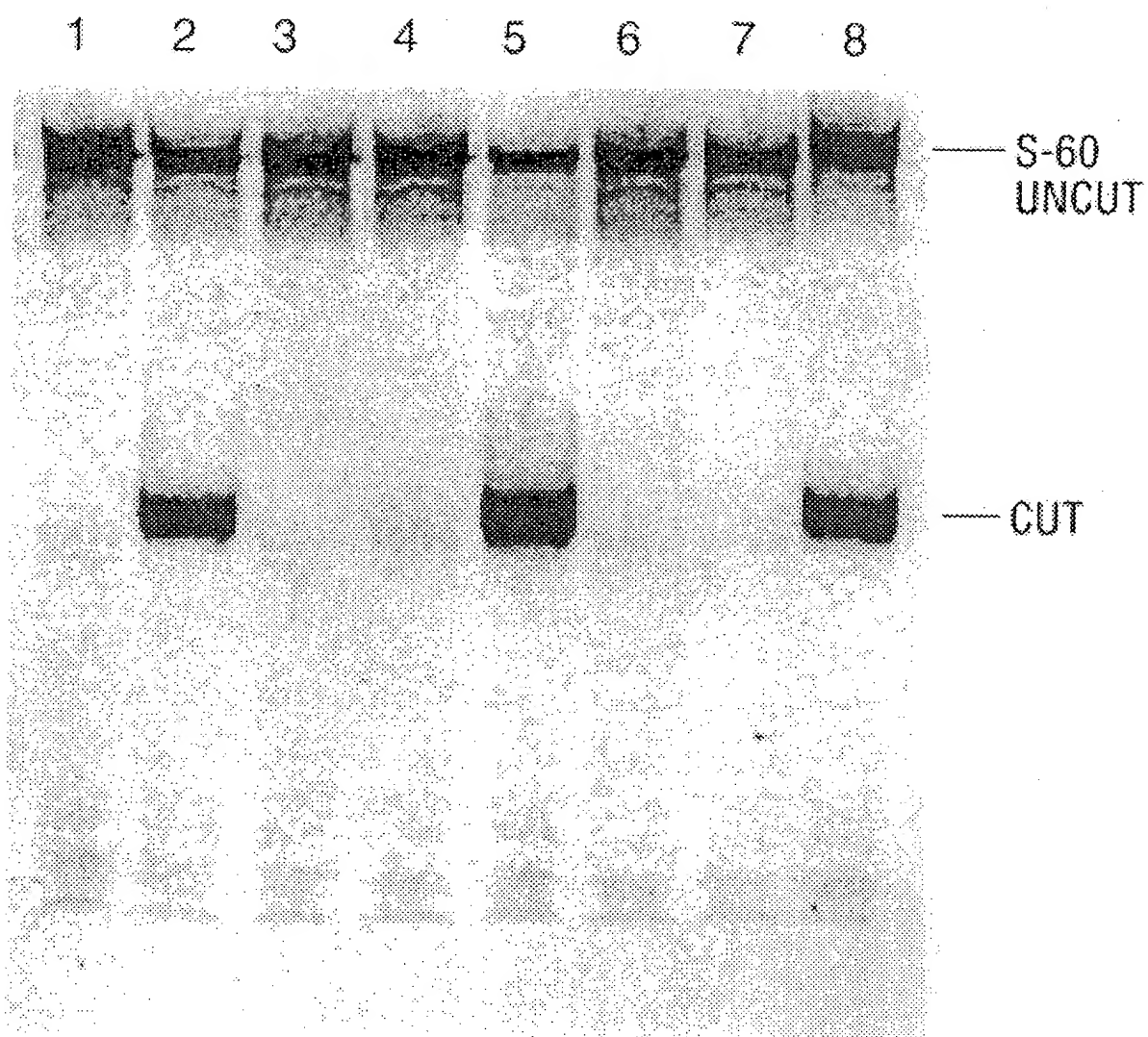


FIG. 62

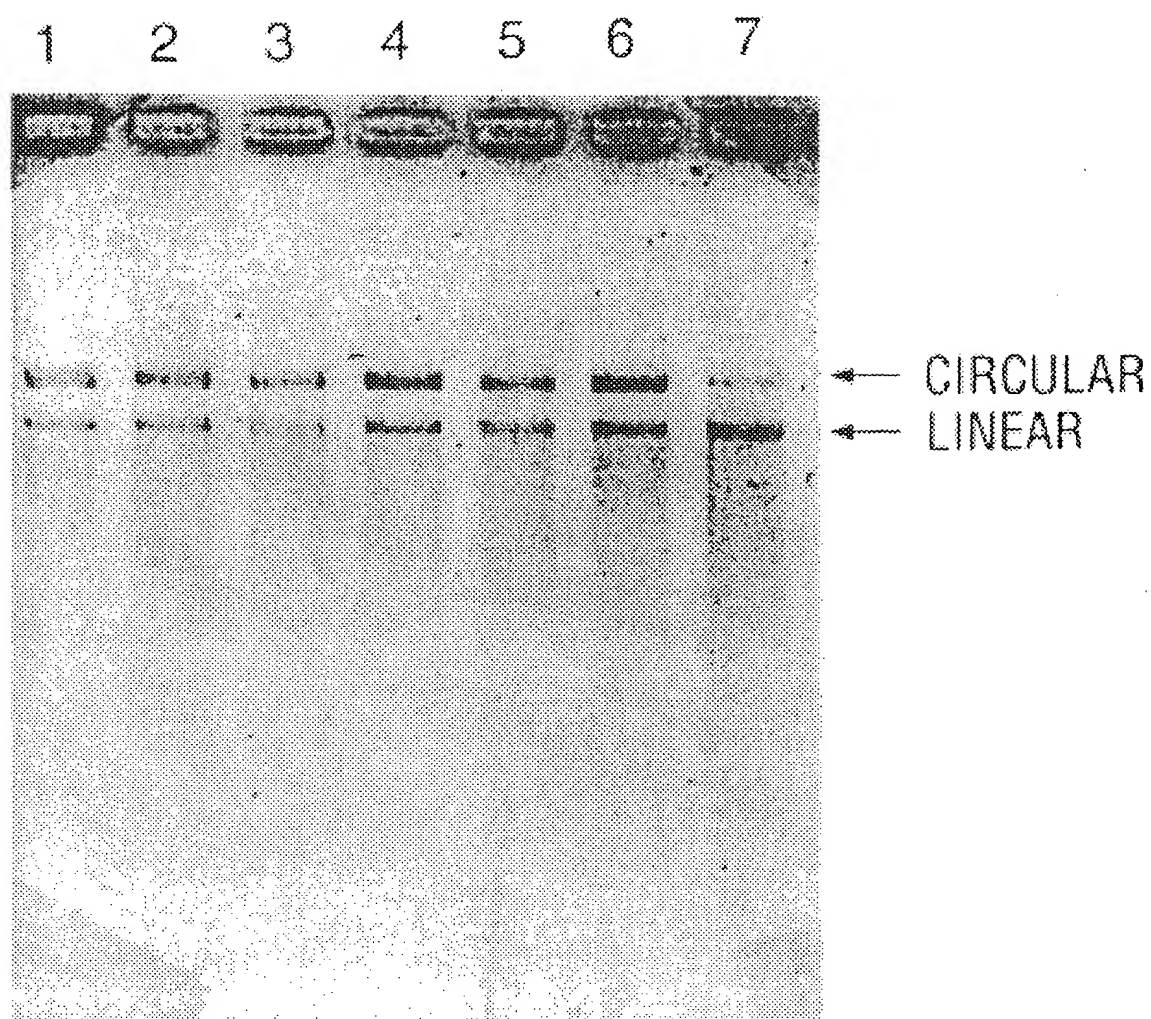


FIG. 63

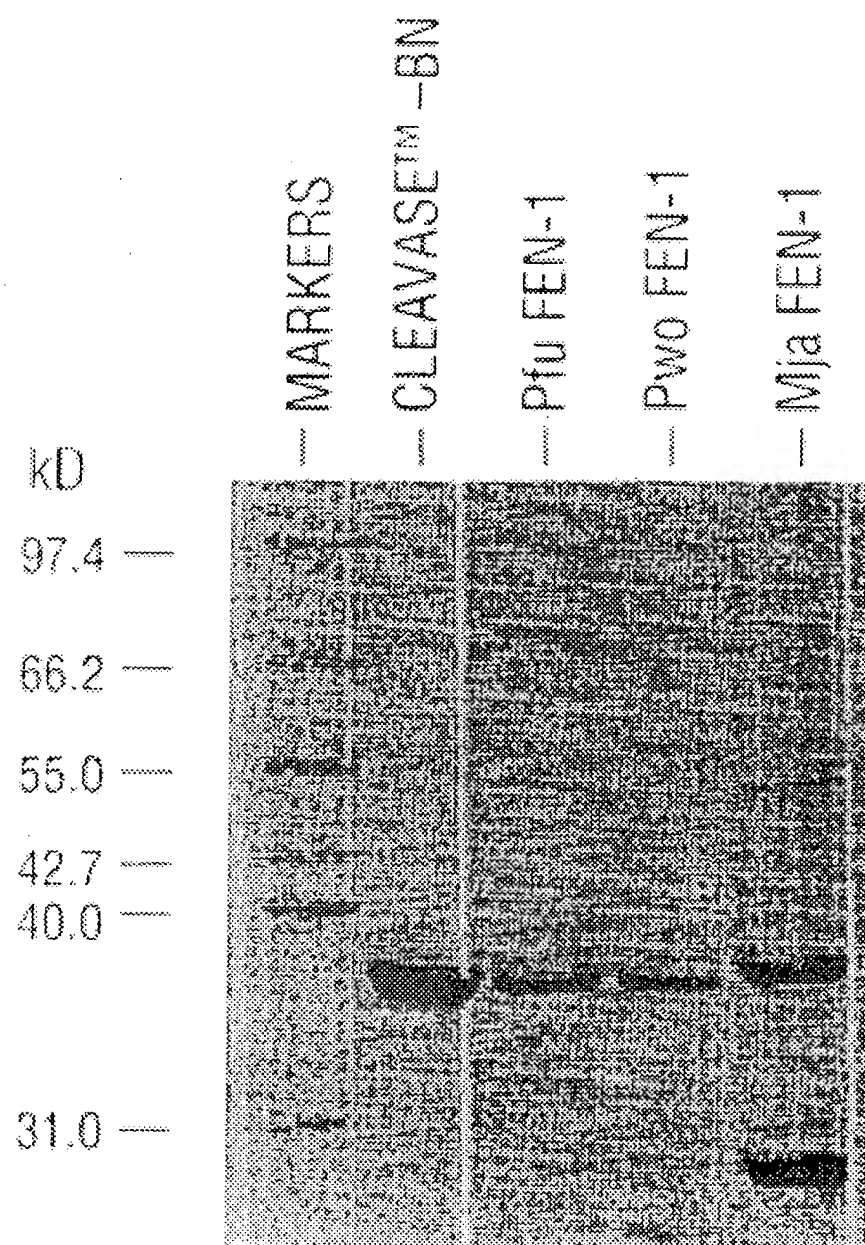


FIG. 64

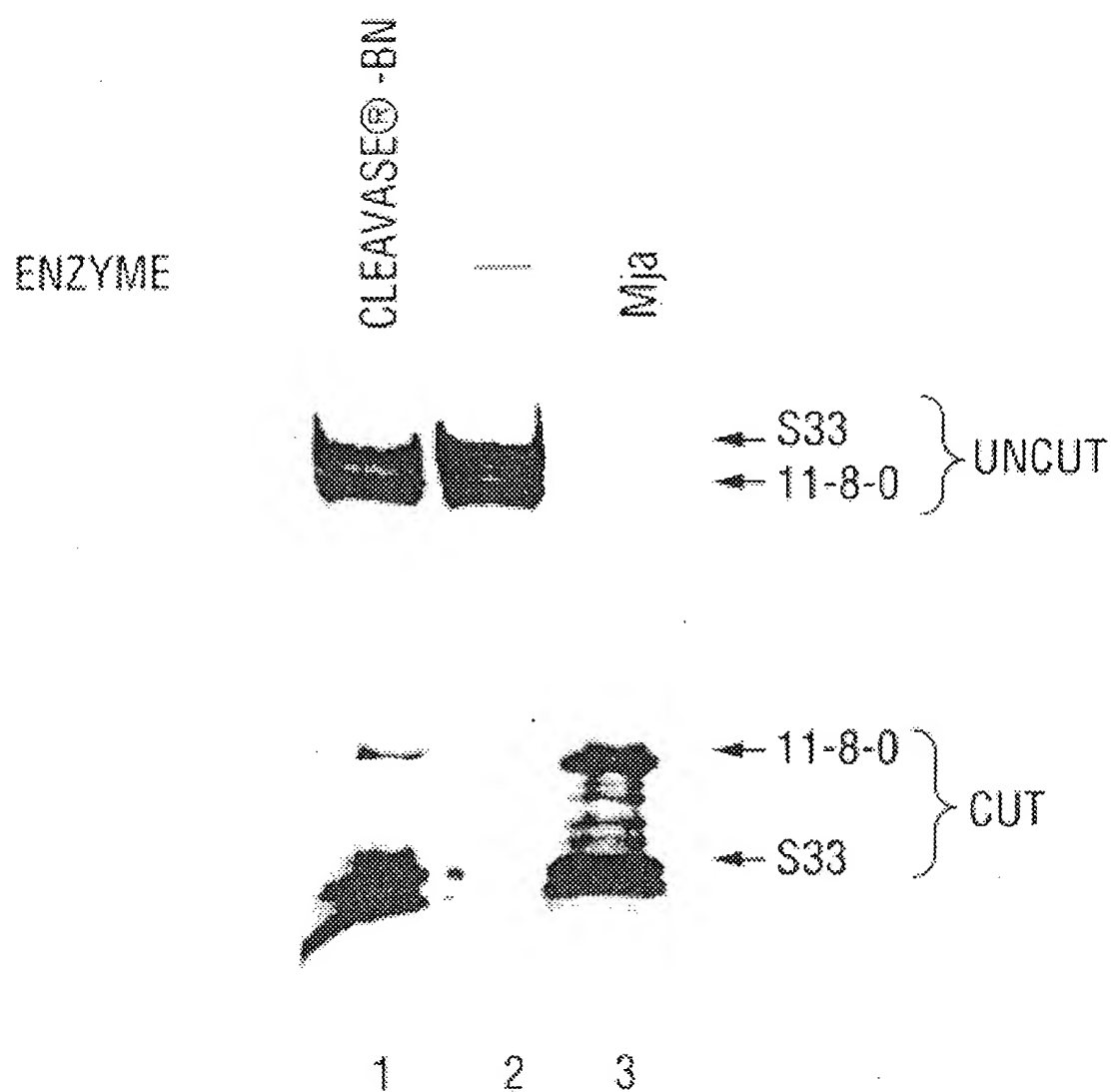
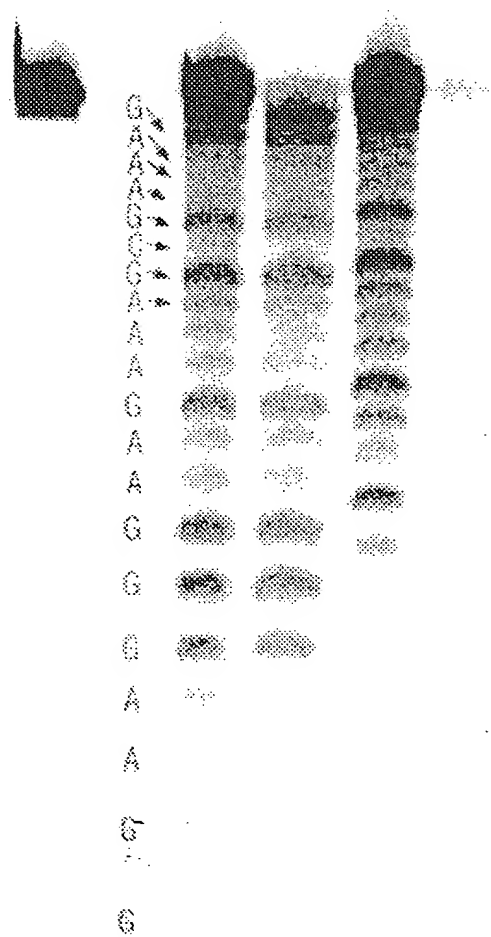


FIG. 65

TERMINAL TRANSFERASE
ALKALINE PHOSPHATASE
THERMAL DEGRADATION



5'-nAGAAggaagggagaaagcgaaagG-3'

FIG. 66

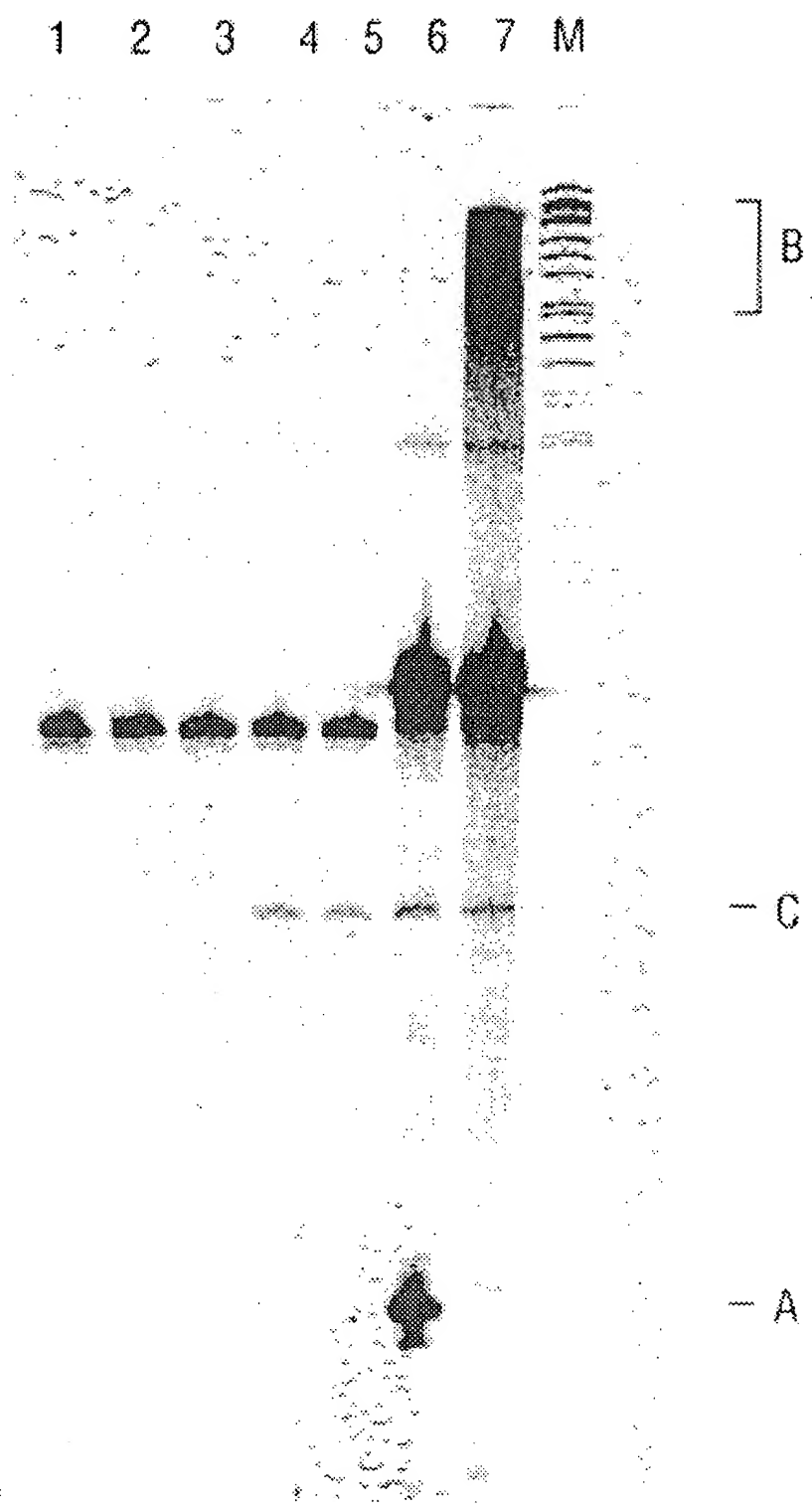


FIG. 67

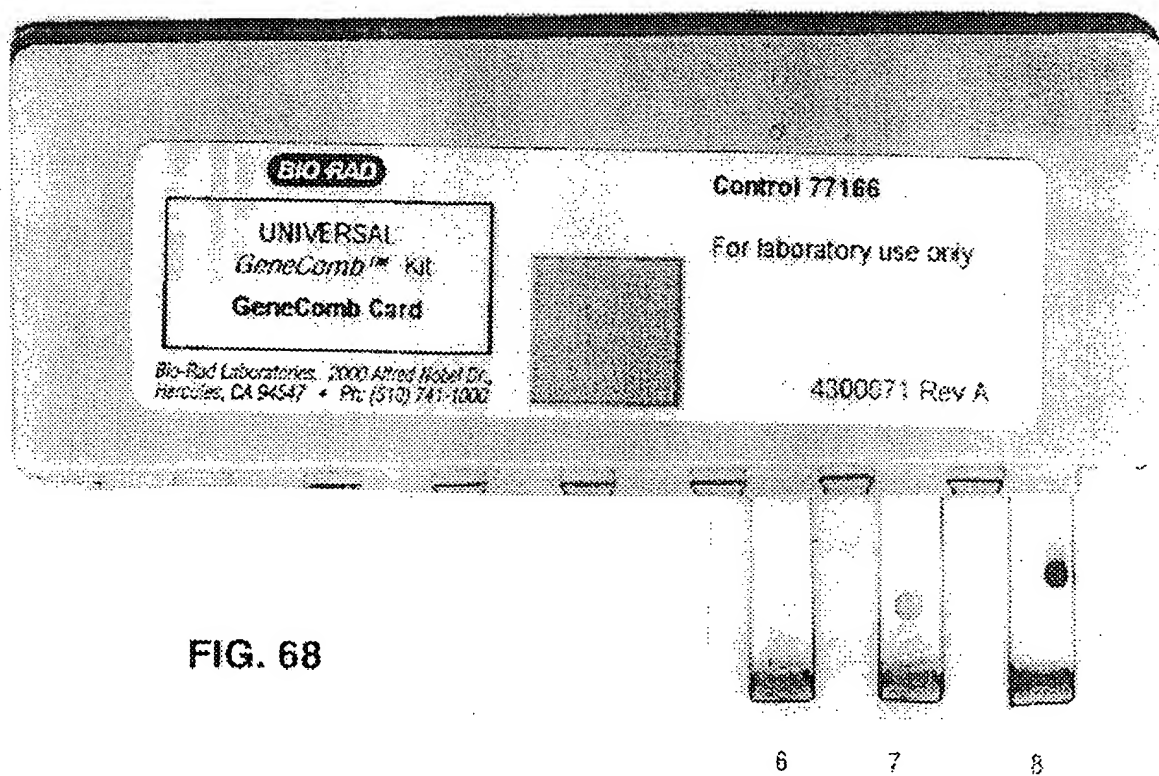


FIG. 68

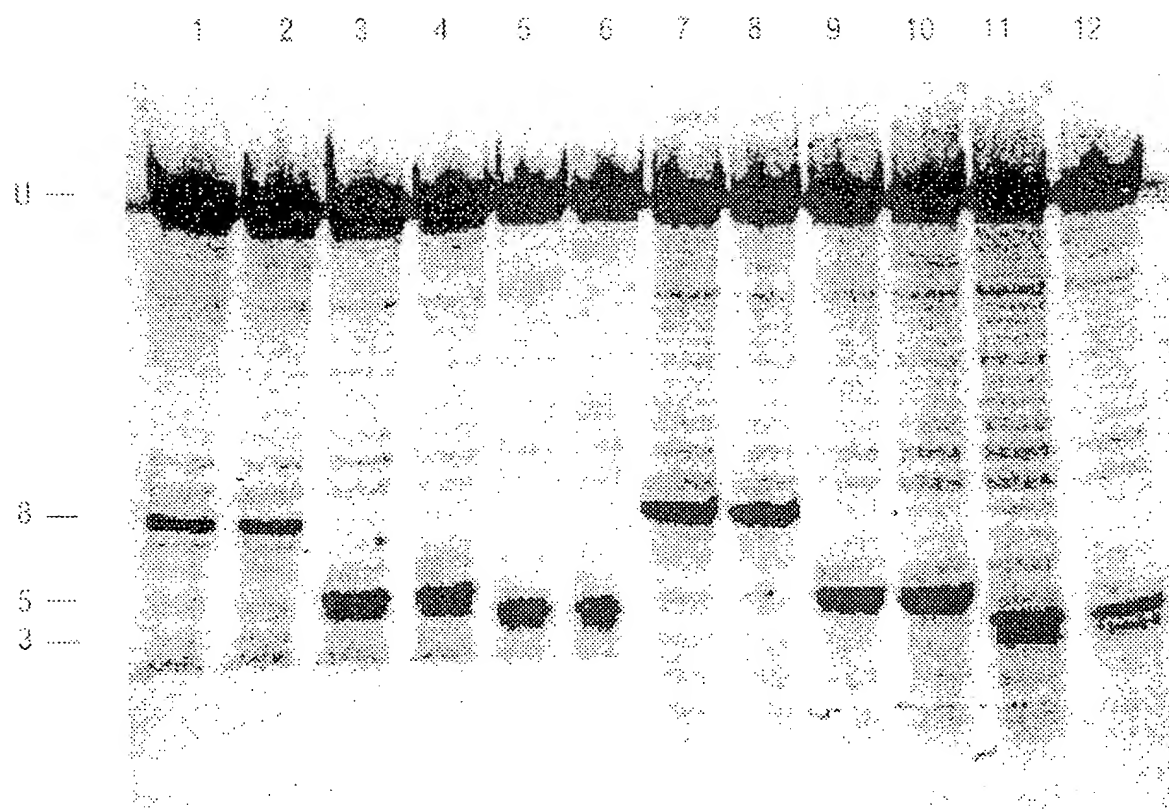


FIG. 69

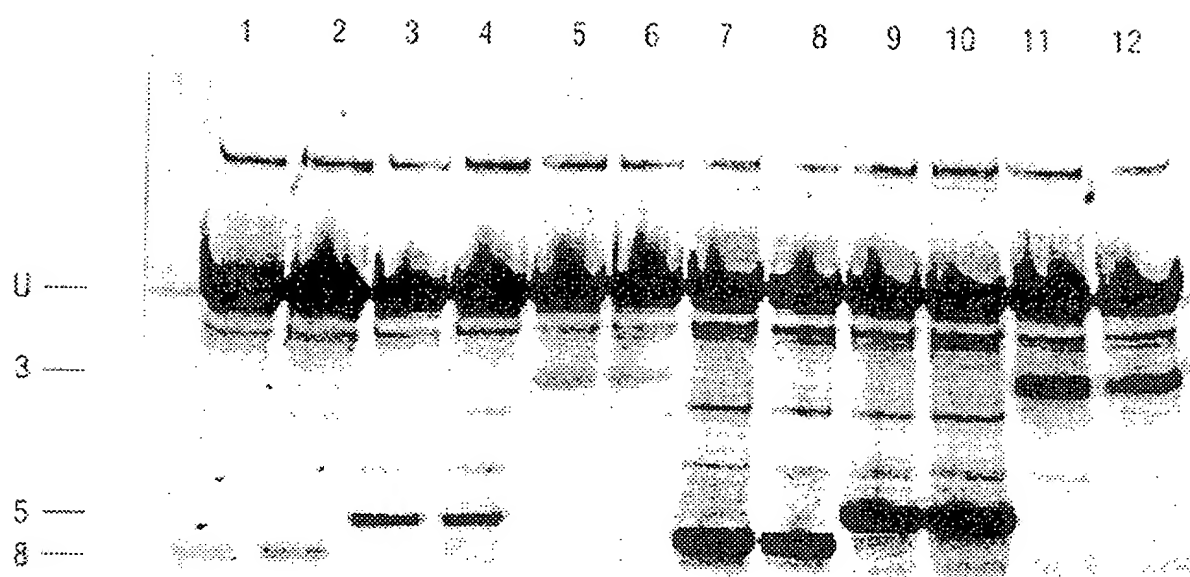


FIG. 70

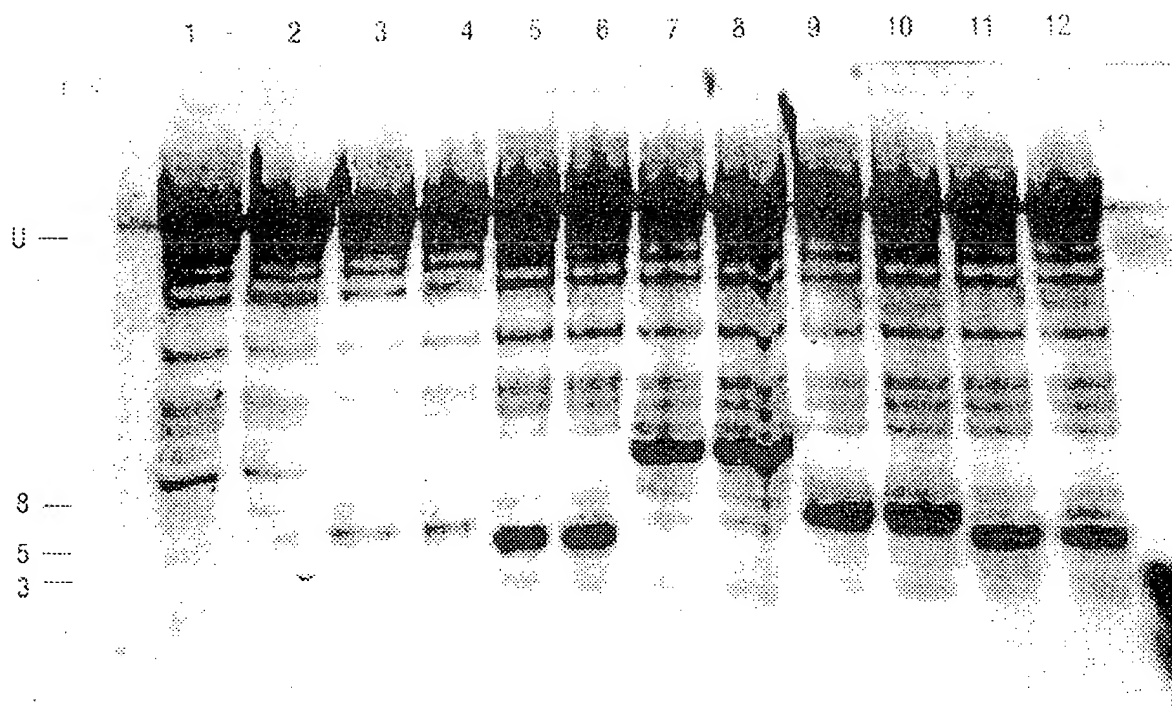


FIG. 71

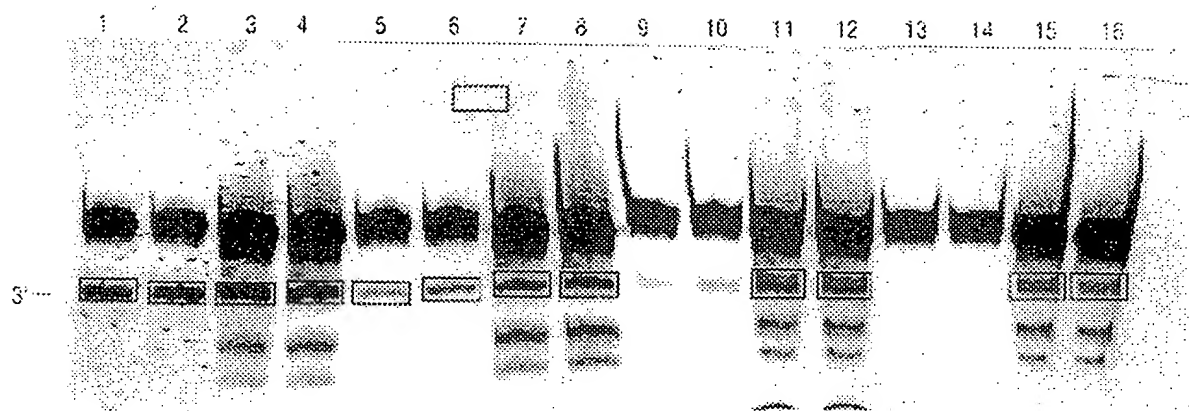


FIG. 72A

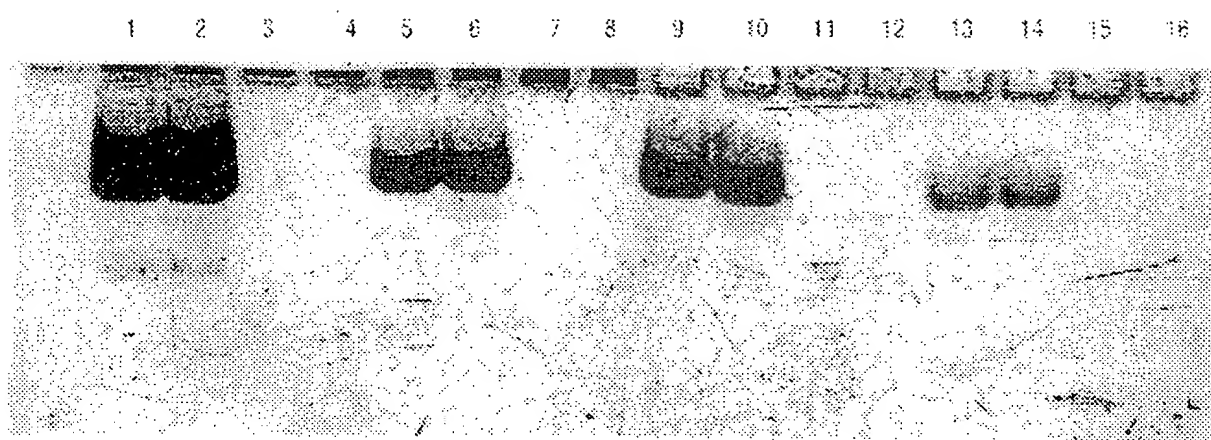
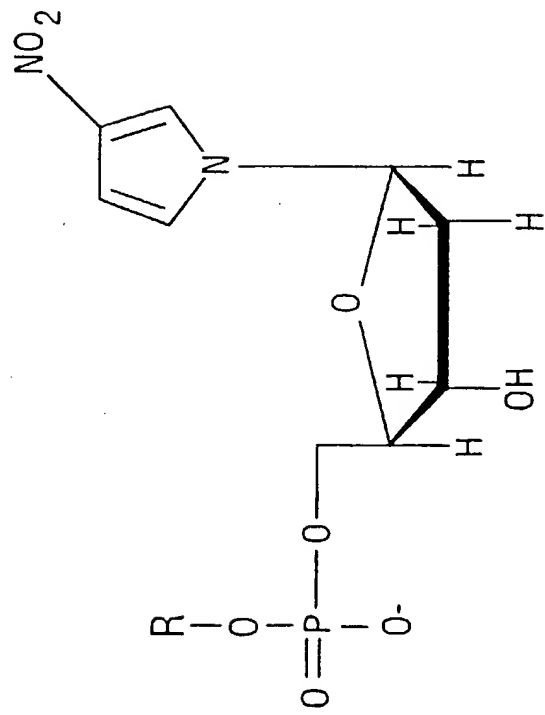
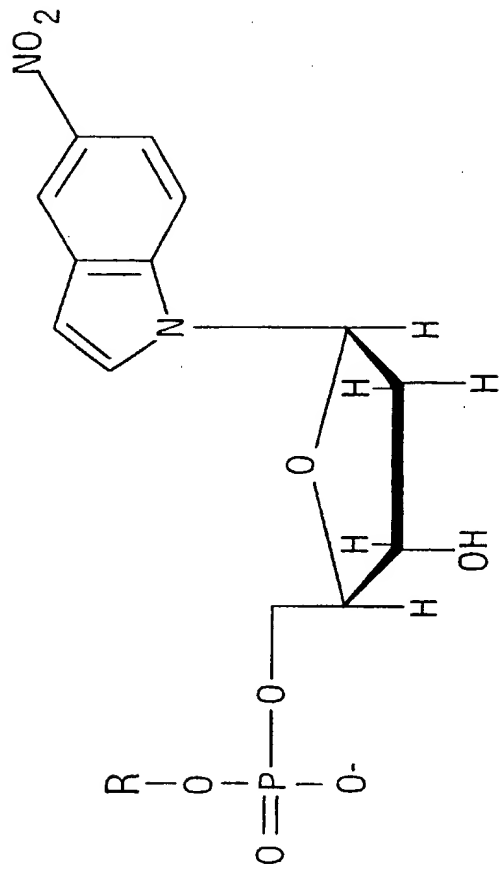


FIG. 72B



3-NITROPYRROLE



5-NITROINDOLE

FIG. 73

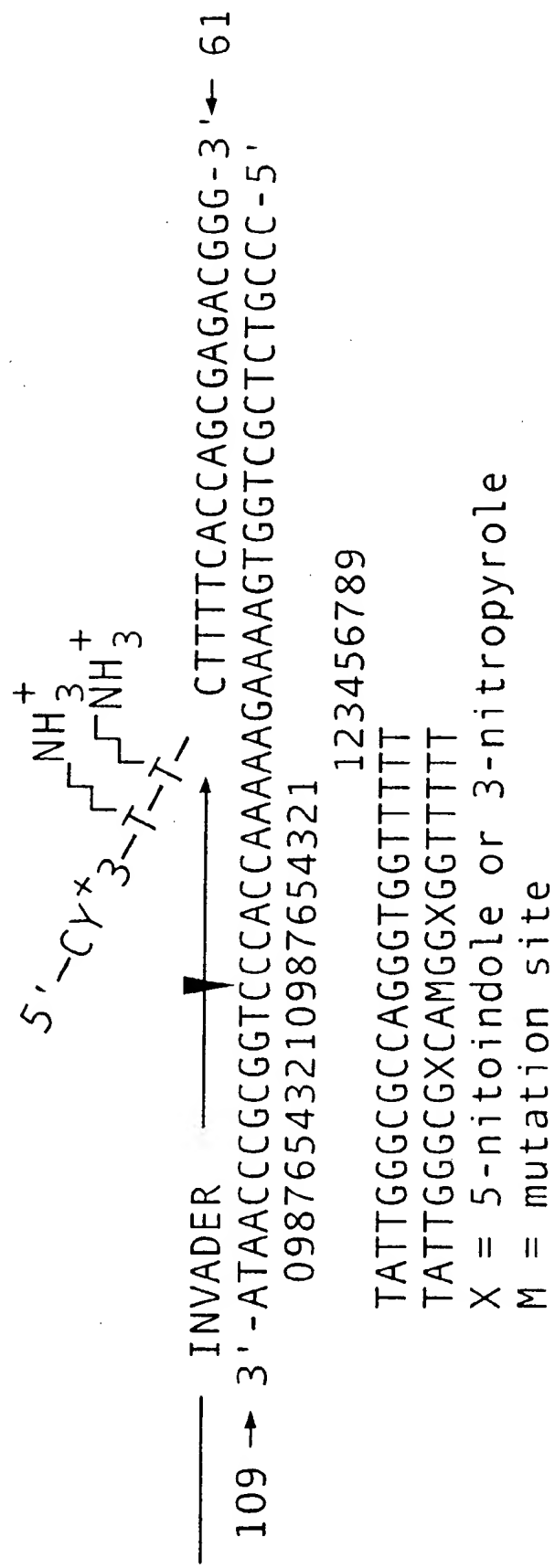


FIG. 74

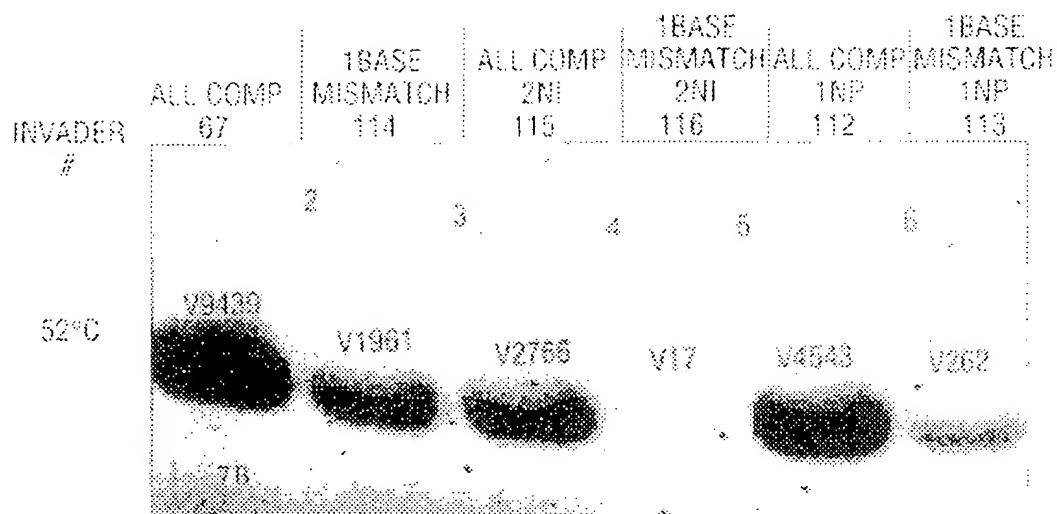


FIG. 75A

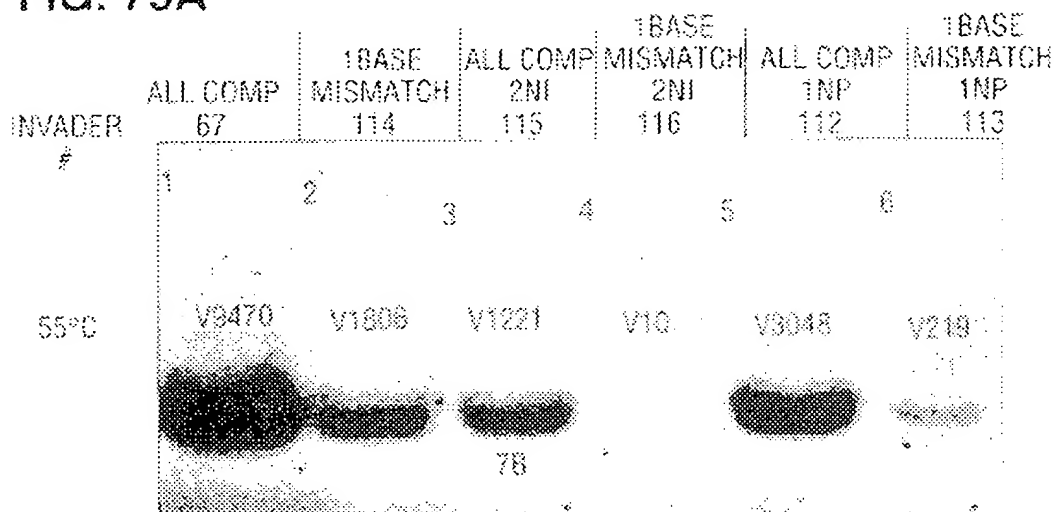


FIG. 75B

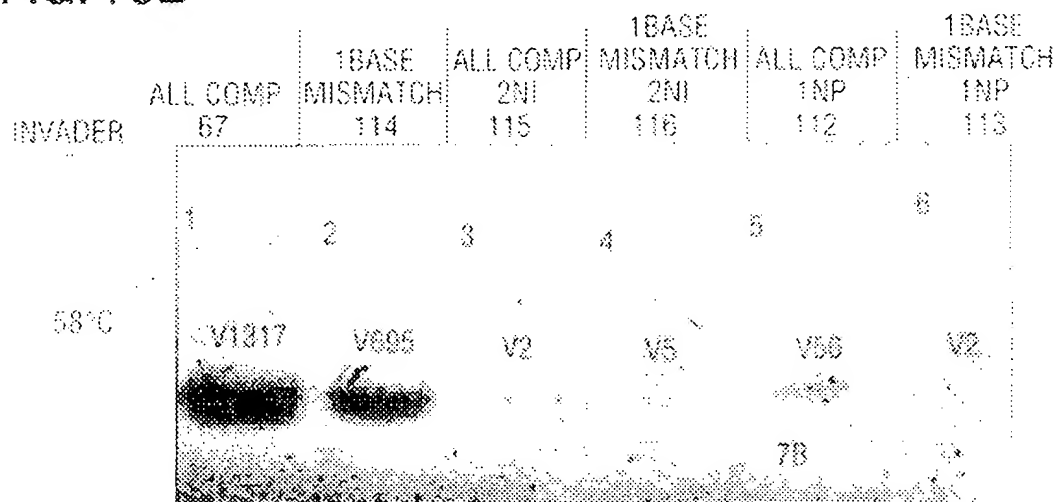


FIG. 75C

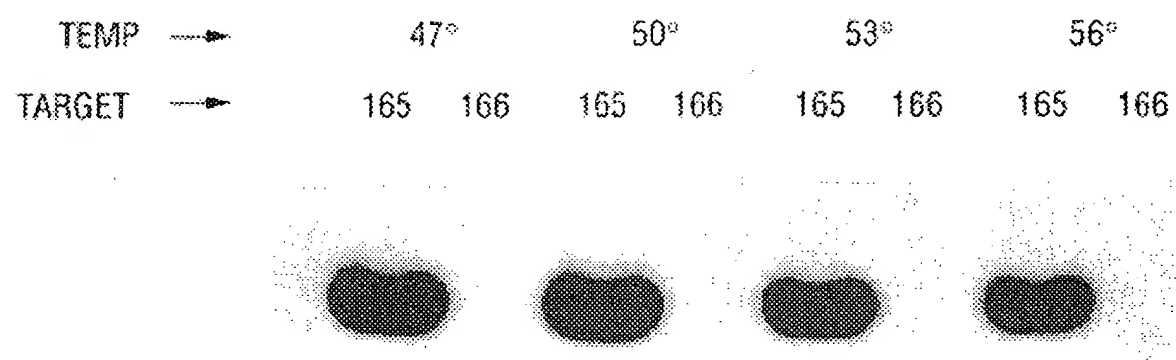


FIG. 77

F1

5' GTTCTCTGCTCTCTGGT 1819
 ↓ ↓
 CGCTGTCTCGCTTGT^G
 GCGACAGAGCGAACA^A
 3' GCTCTCTGGT

FIG. 78A

F1

5' GTTCTCTGCTCTCTGGT 2122
 ↓ ↓
 CGCT GTCTCGCTTGT^G
 3' GCTCTCTGGTGCGACAGAGCGAACA^A
 5' CGAGAGACCACGCT^G
 P15

FIG. 78B

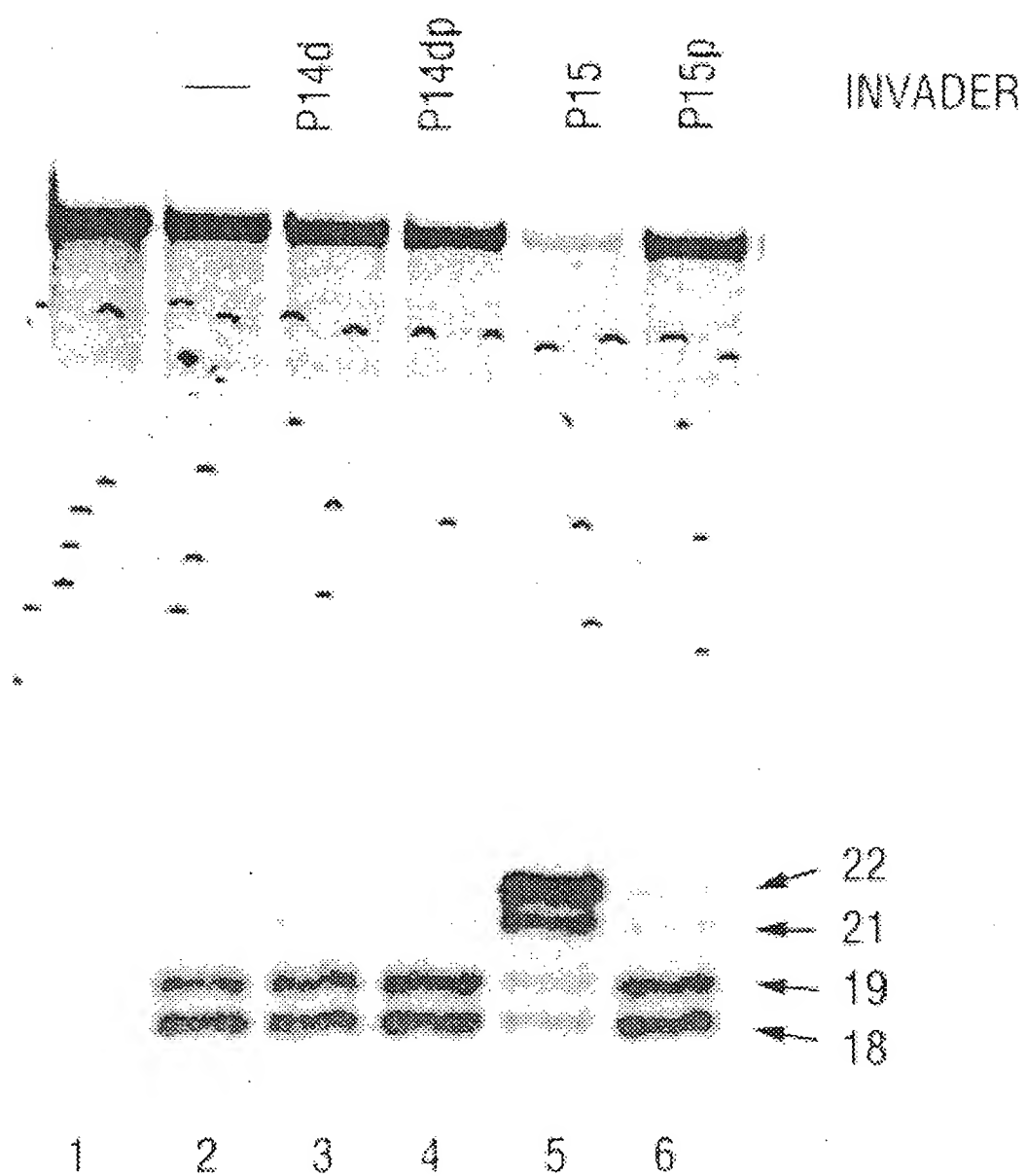


FIG. 78C

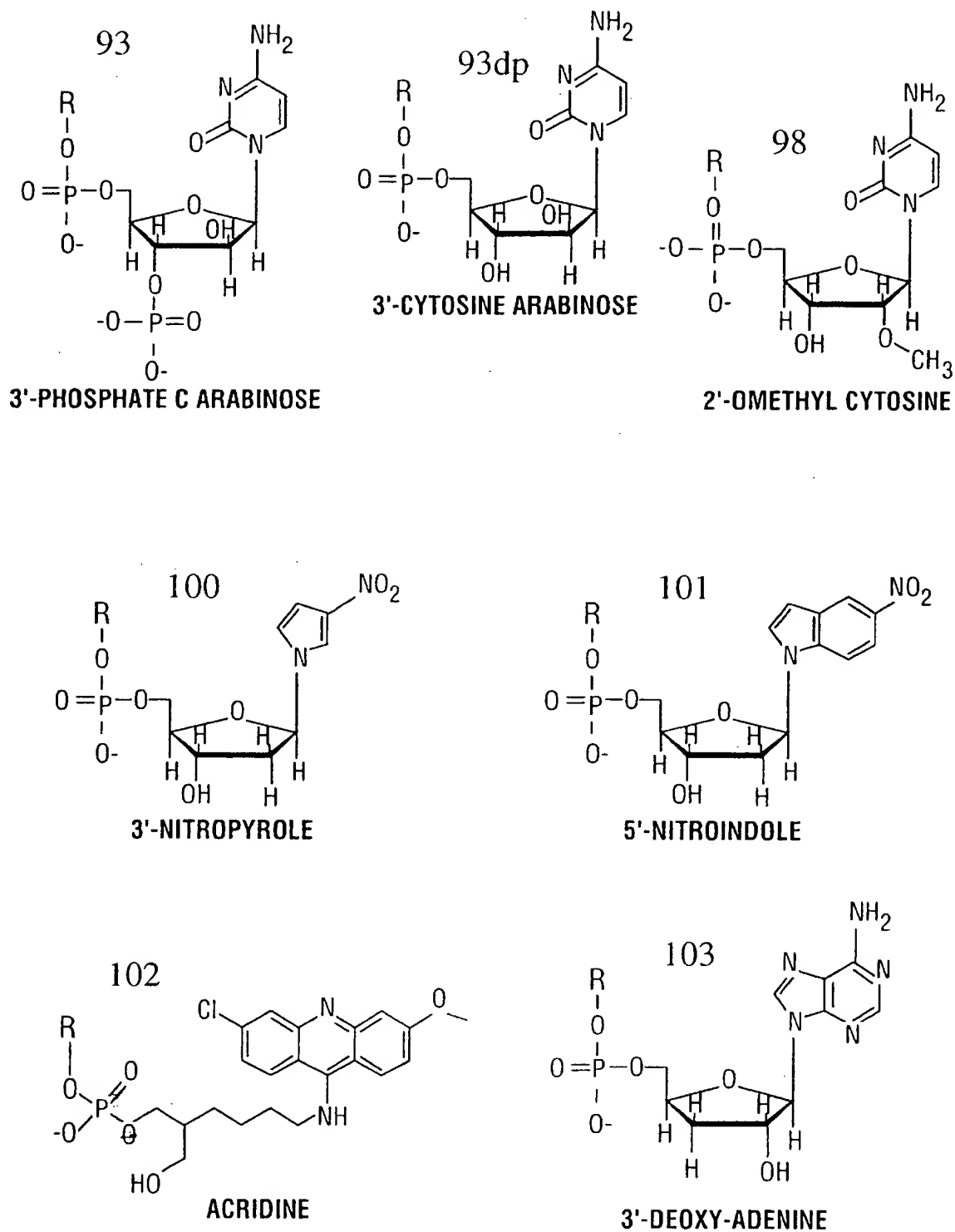
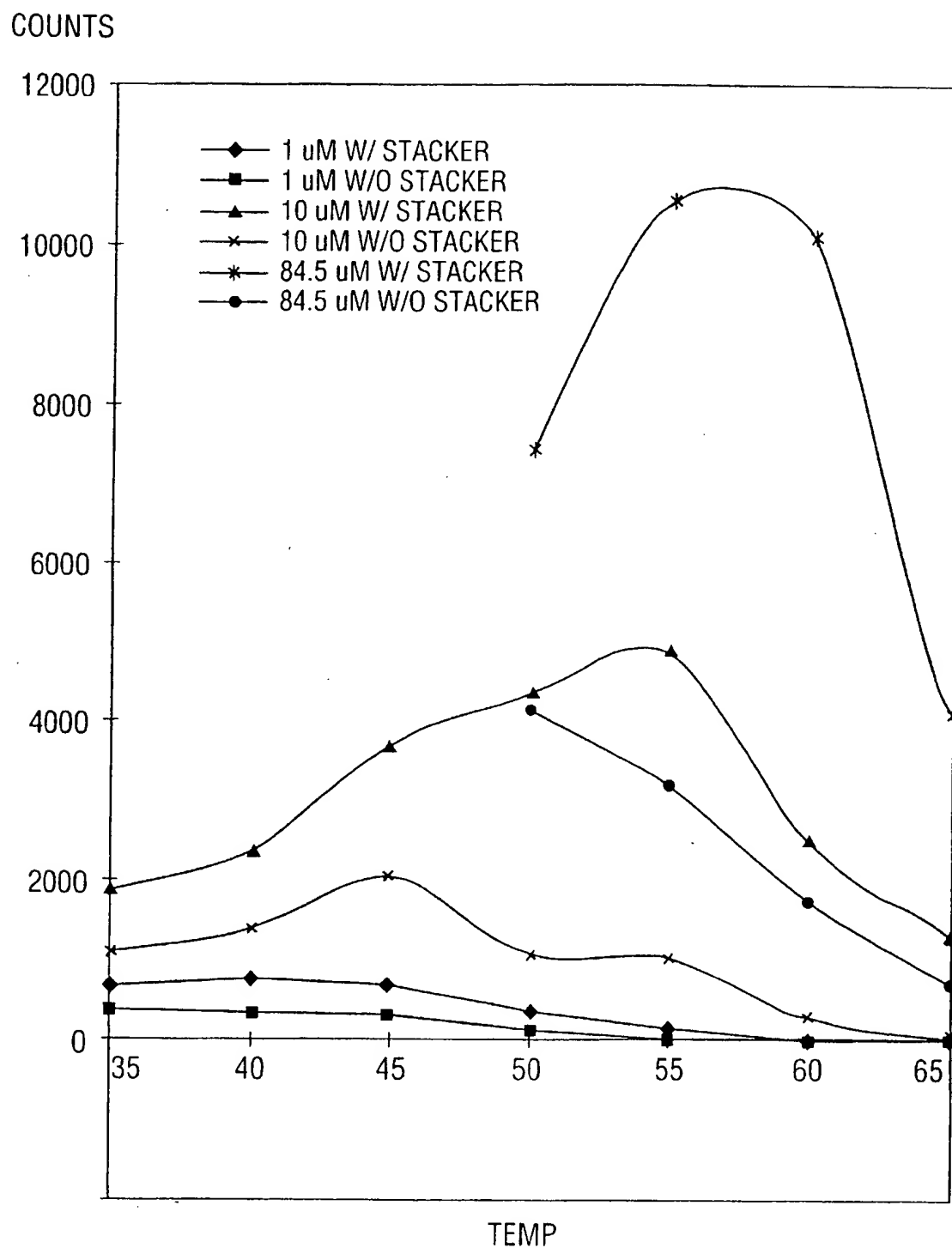


FIG. 79



CONCENTRATION OF PROBE W/ AND W/O STACKER vs TEMP

FIG. 80

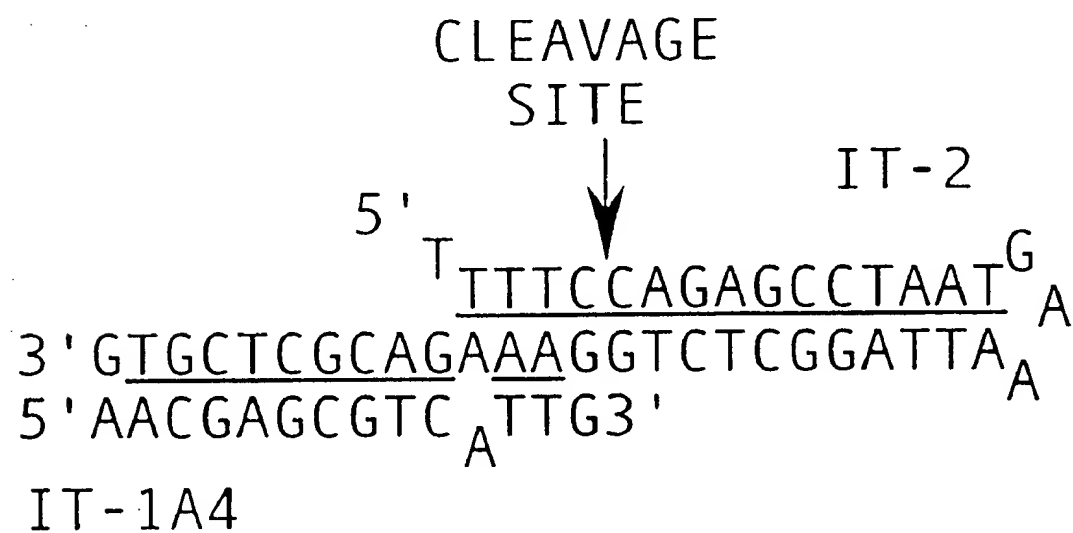
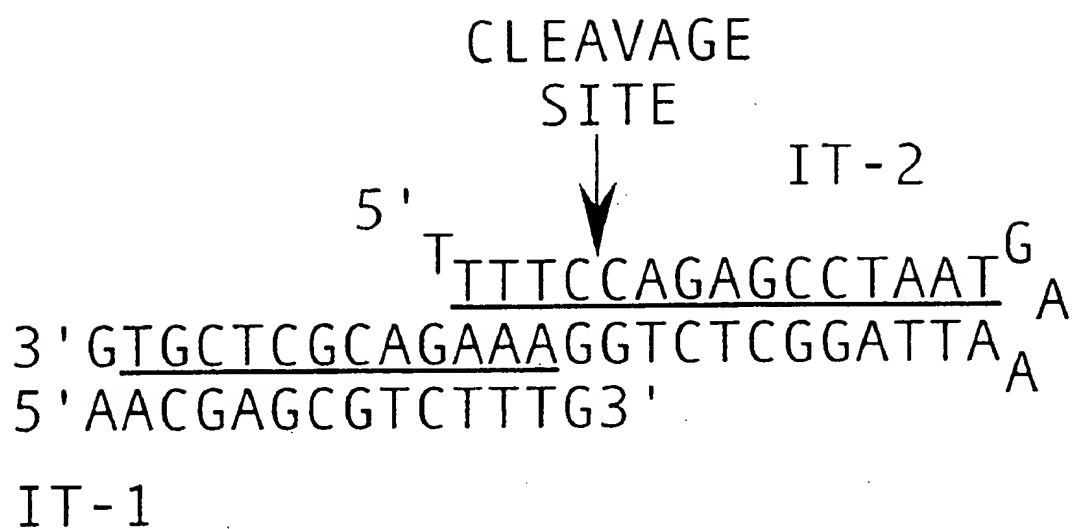


FIG. 81

1 2 3 4



— UNCUT



FIG. 82

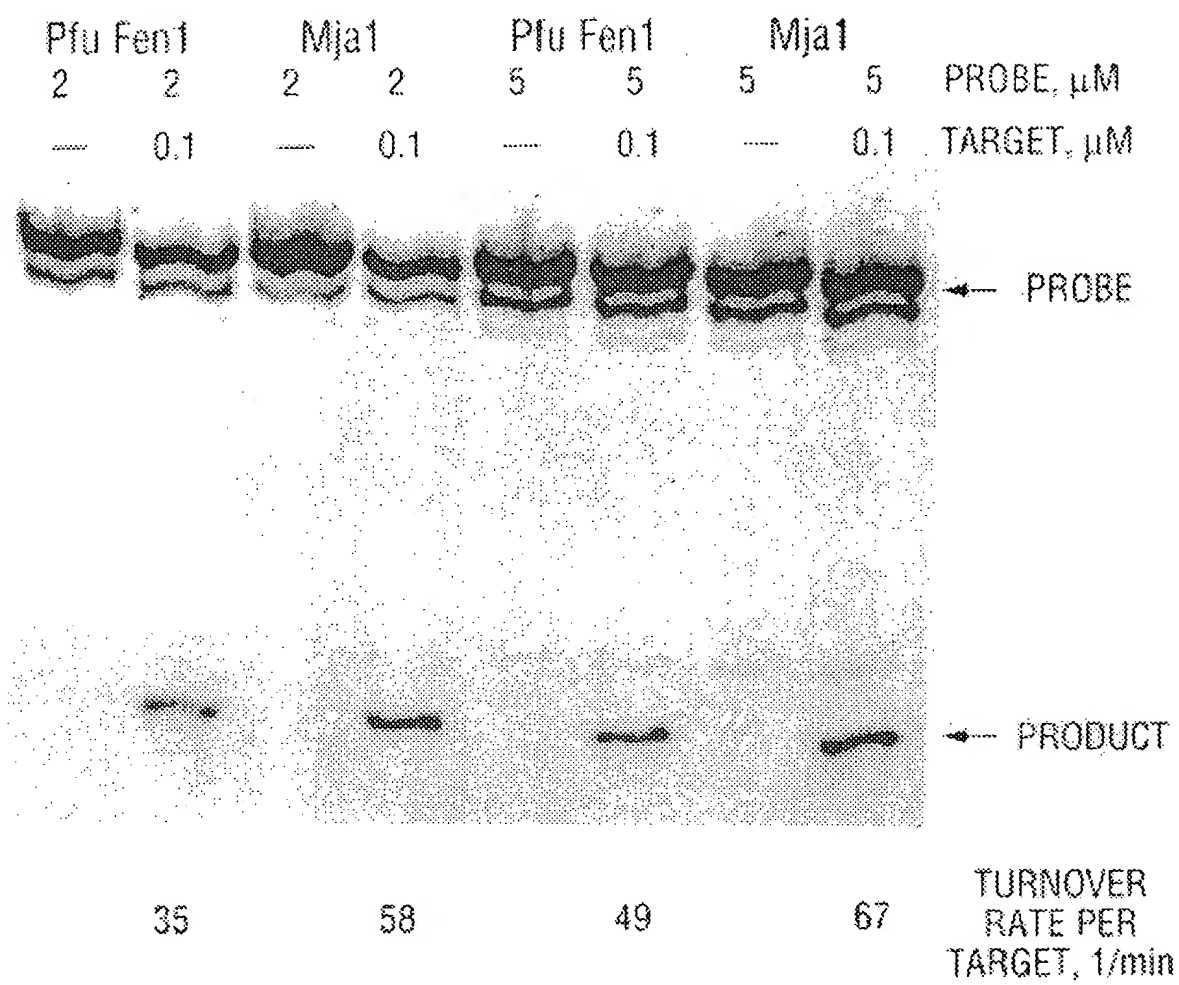


FIG. 83

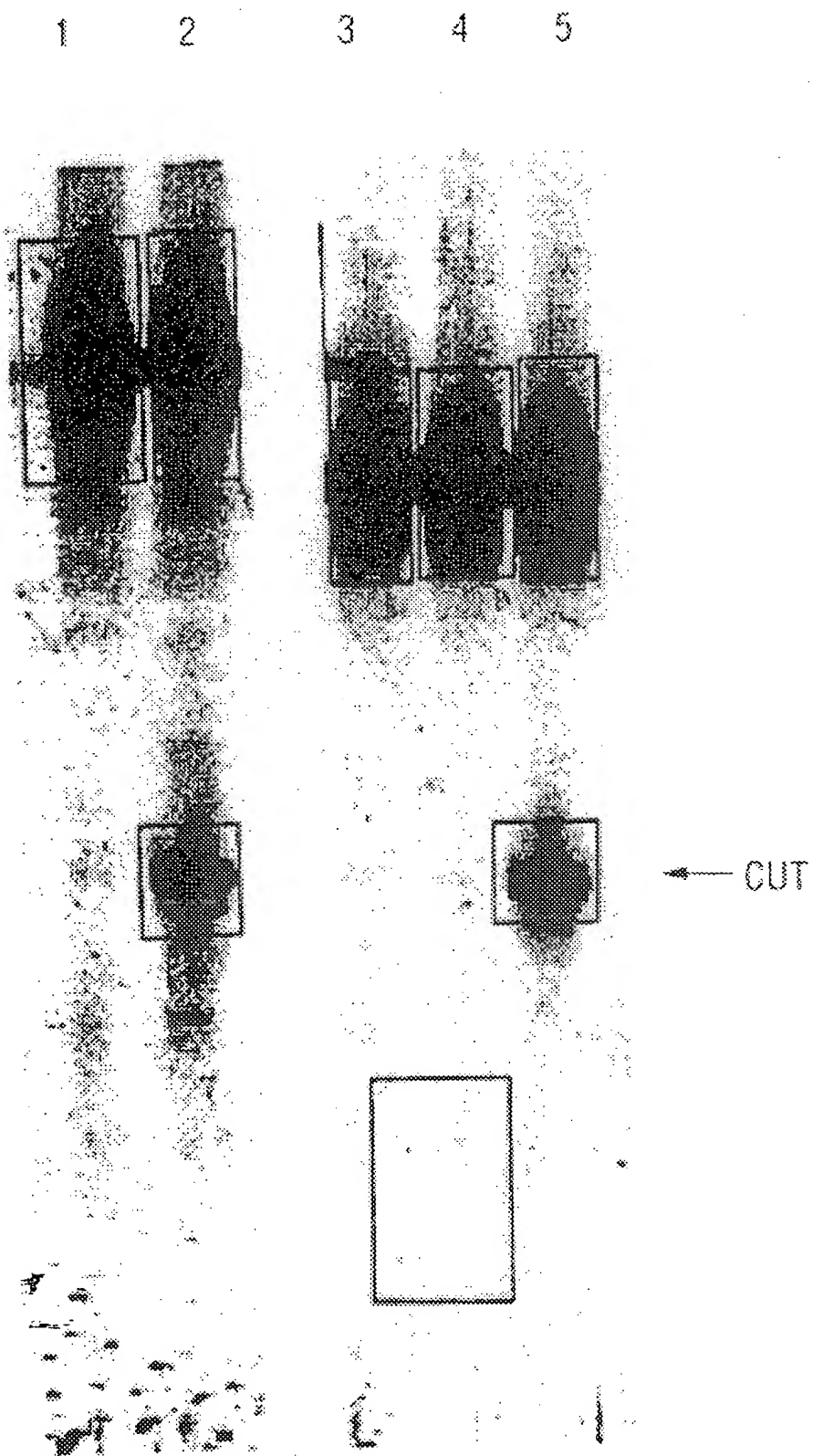
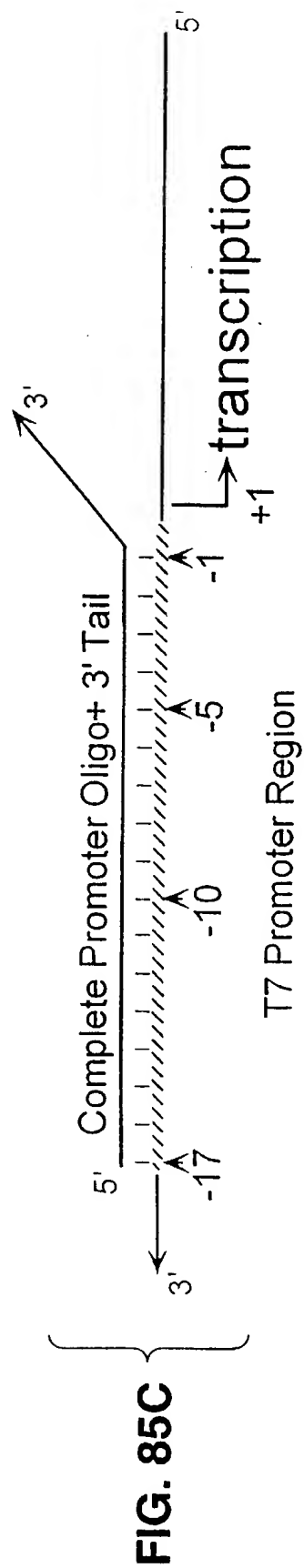
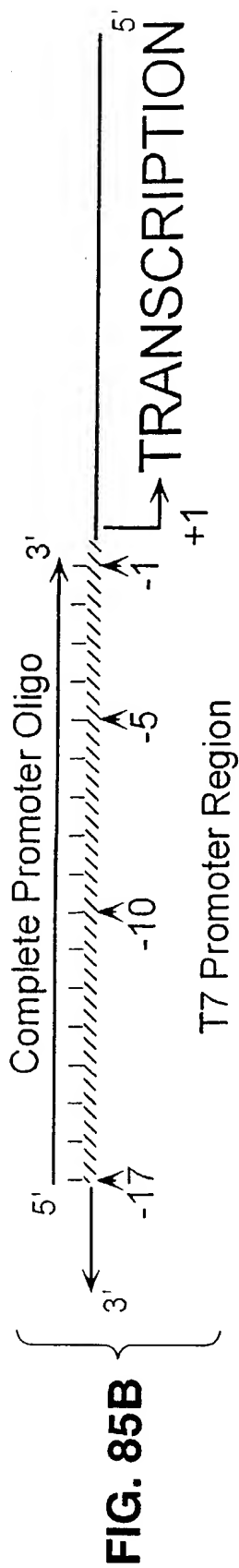
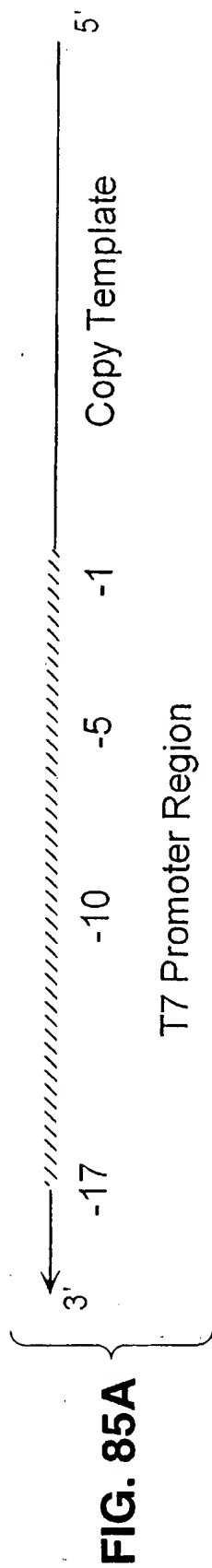
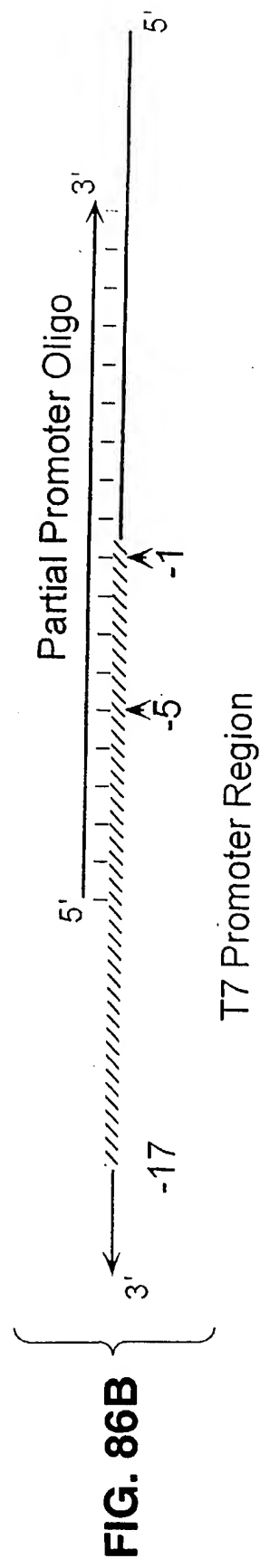
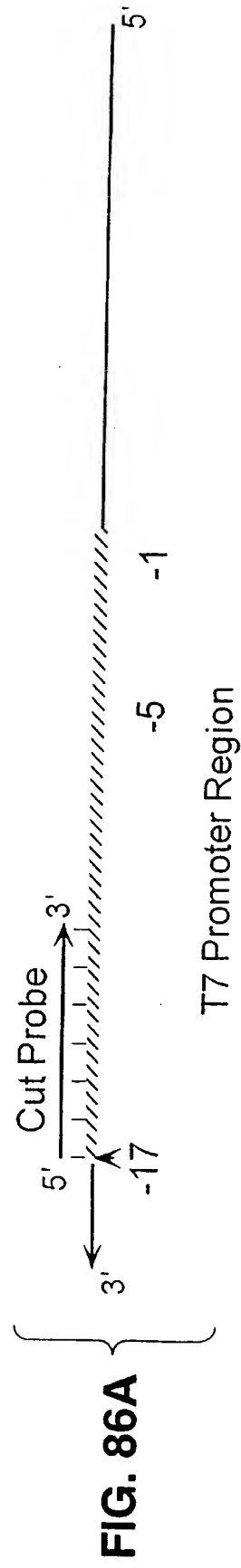


FIG. 84





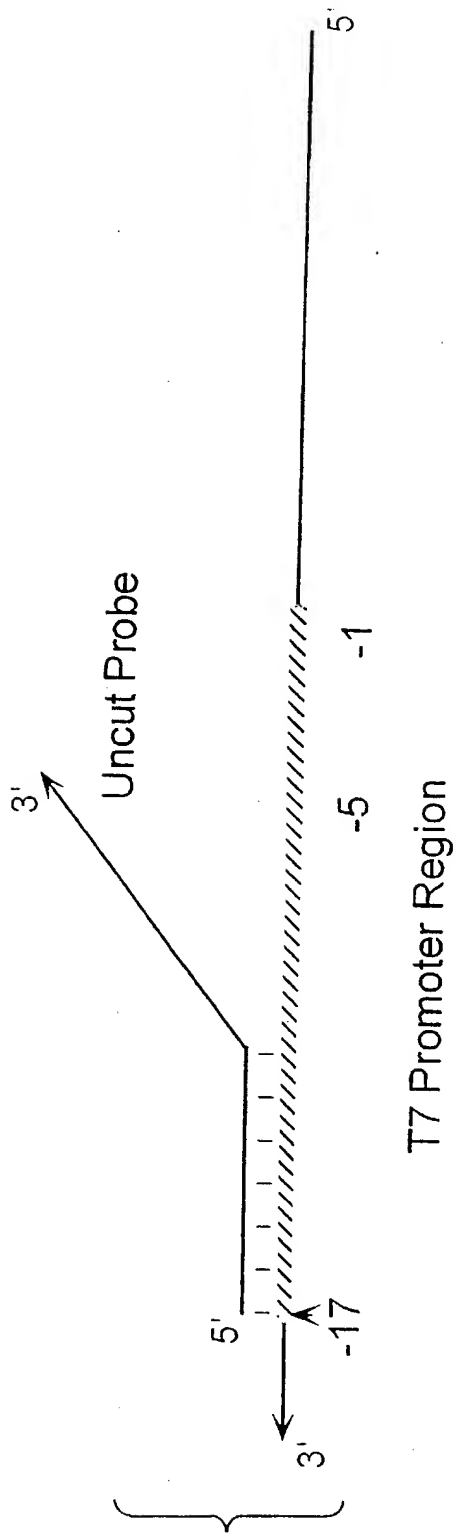


FIG. 86C

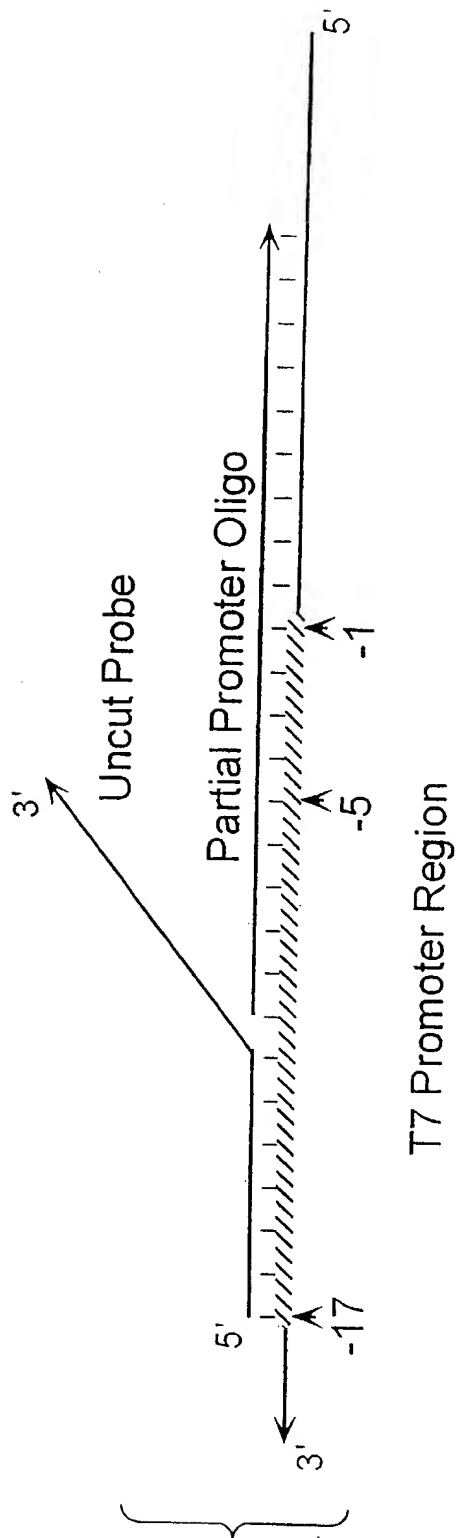


FIG. 86D

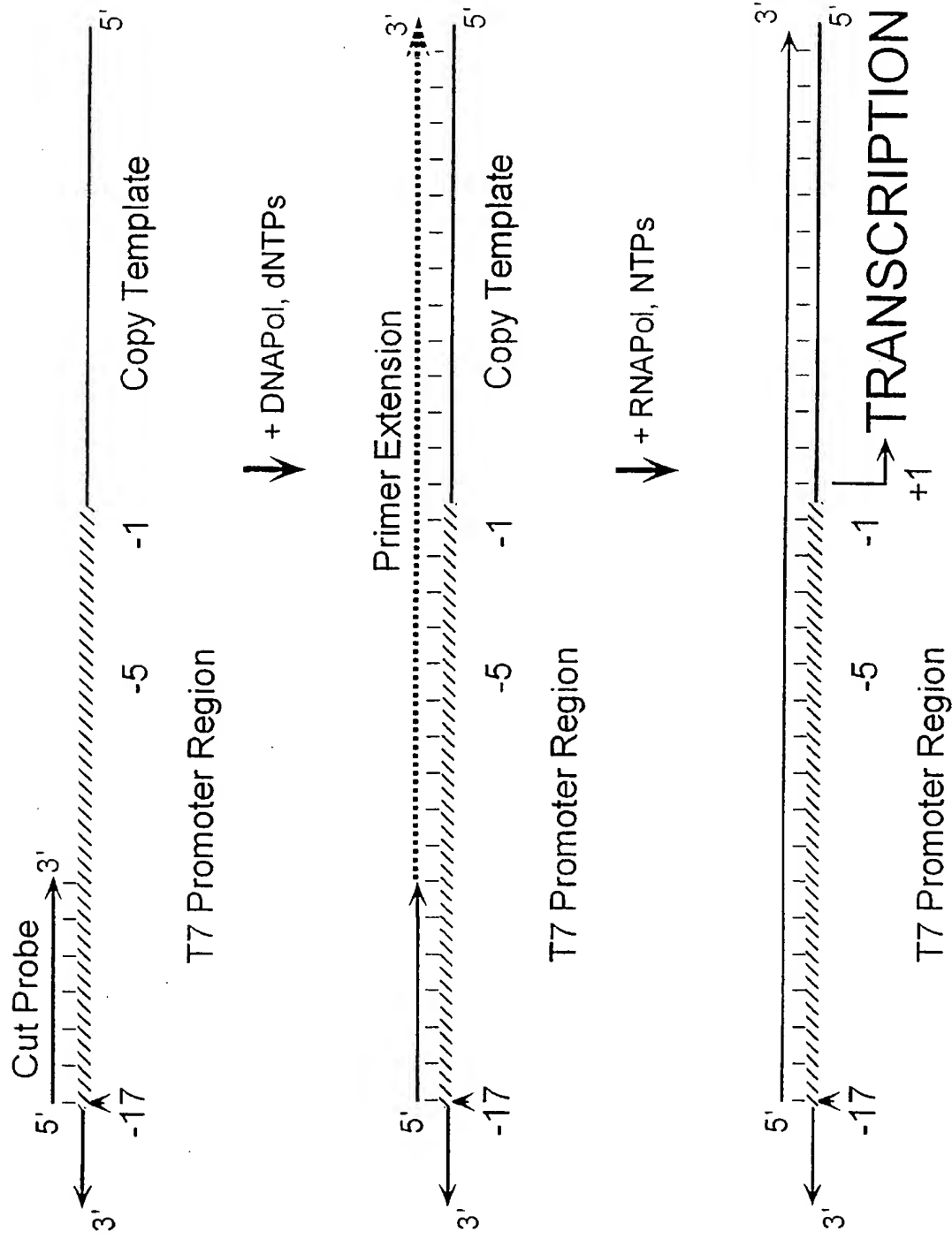
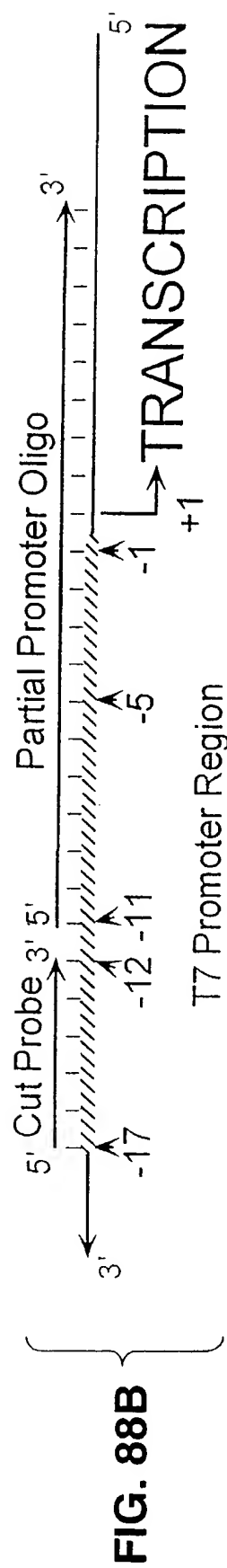
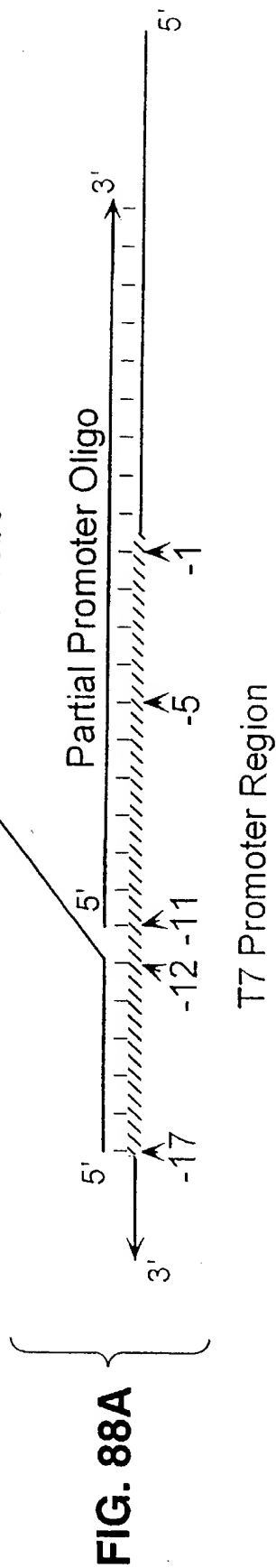


FIG. 87



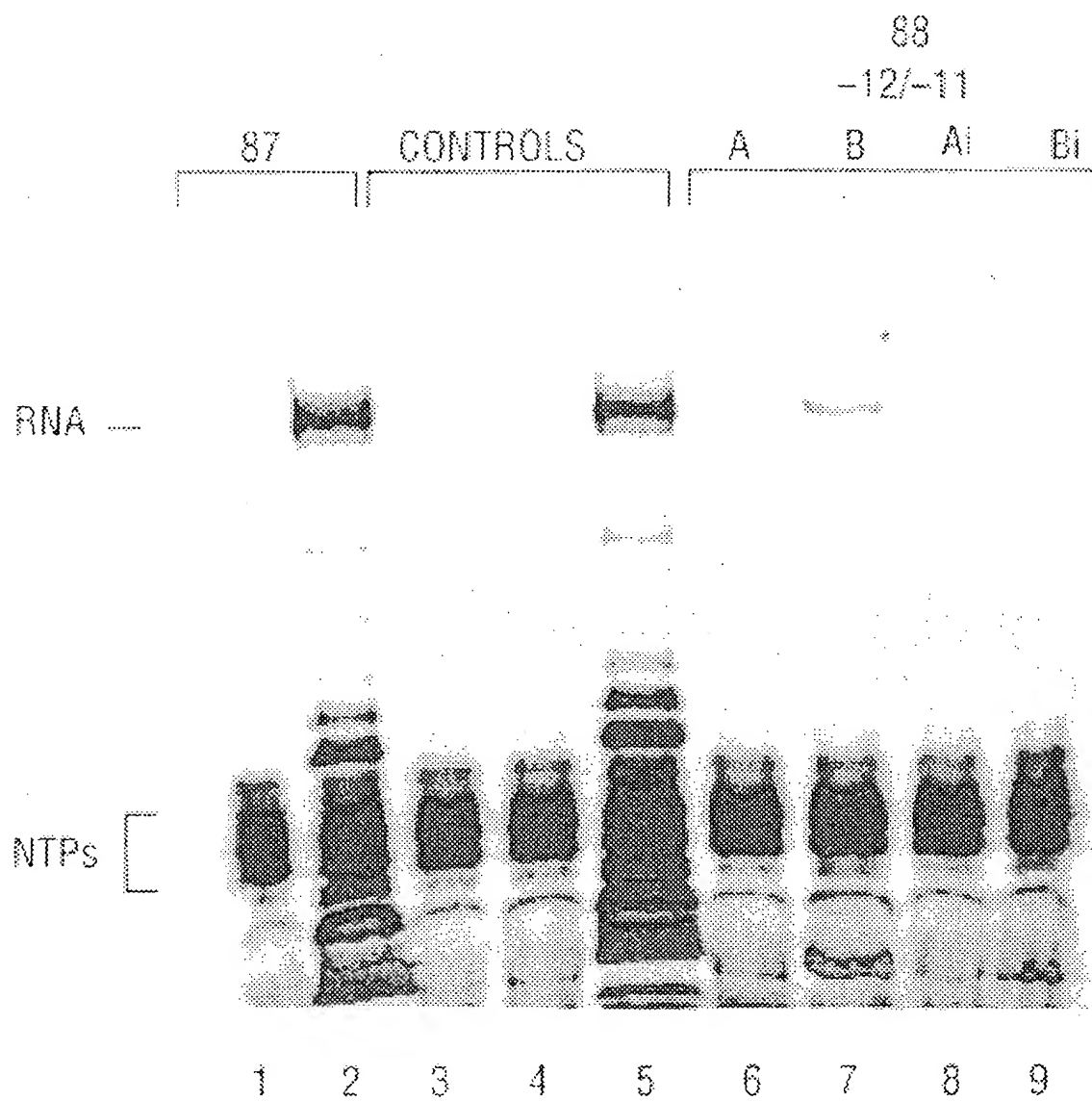
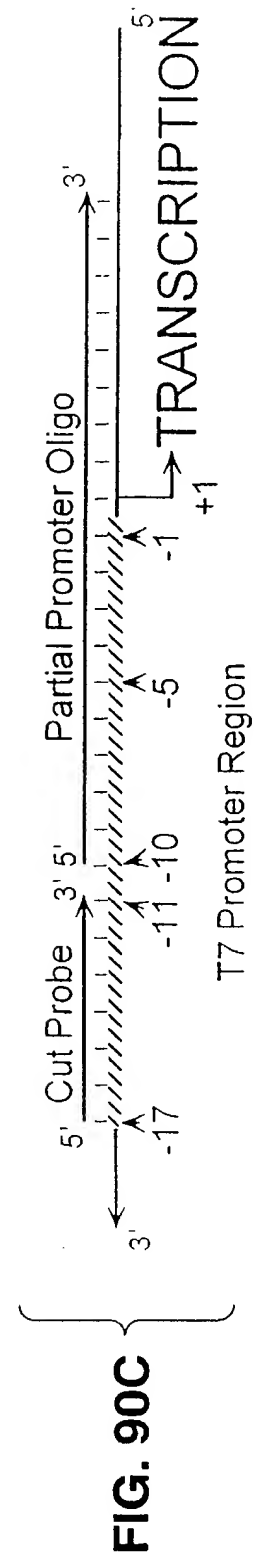
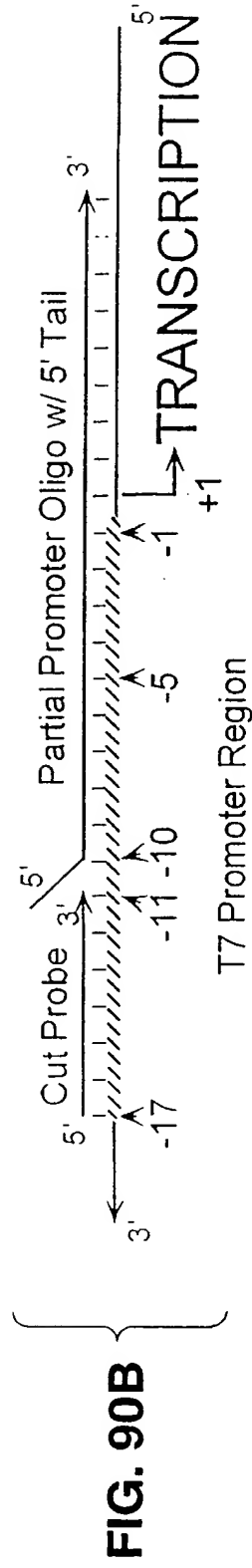
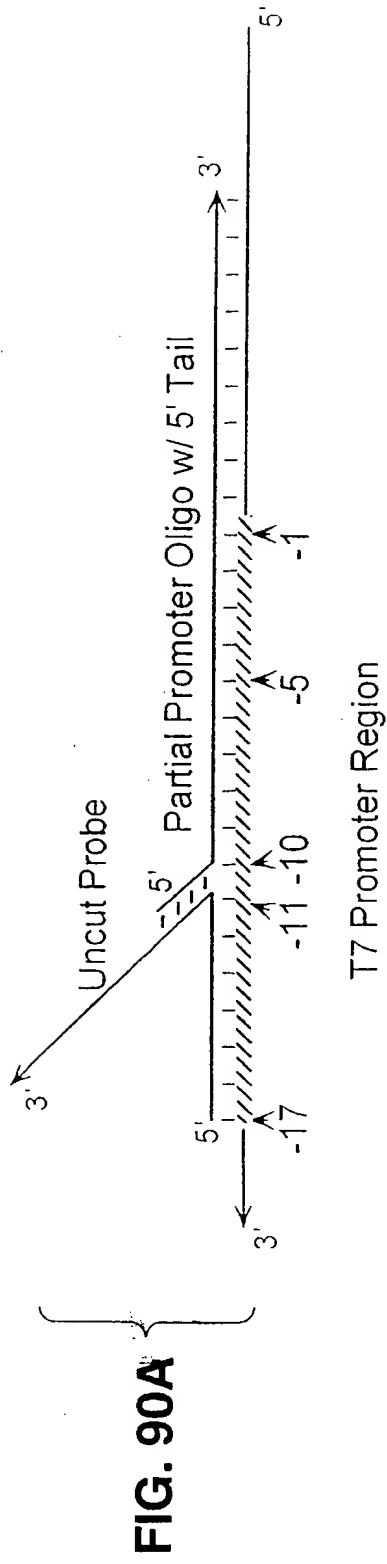


FIG. 89



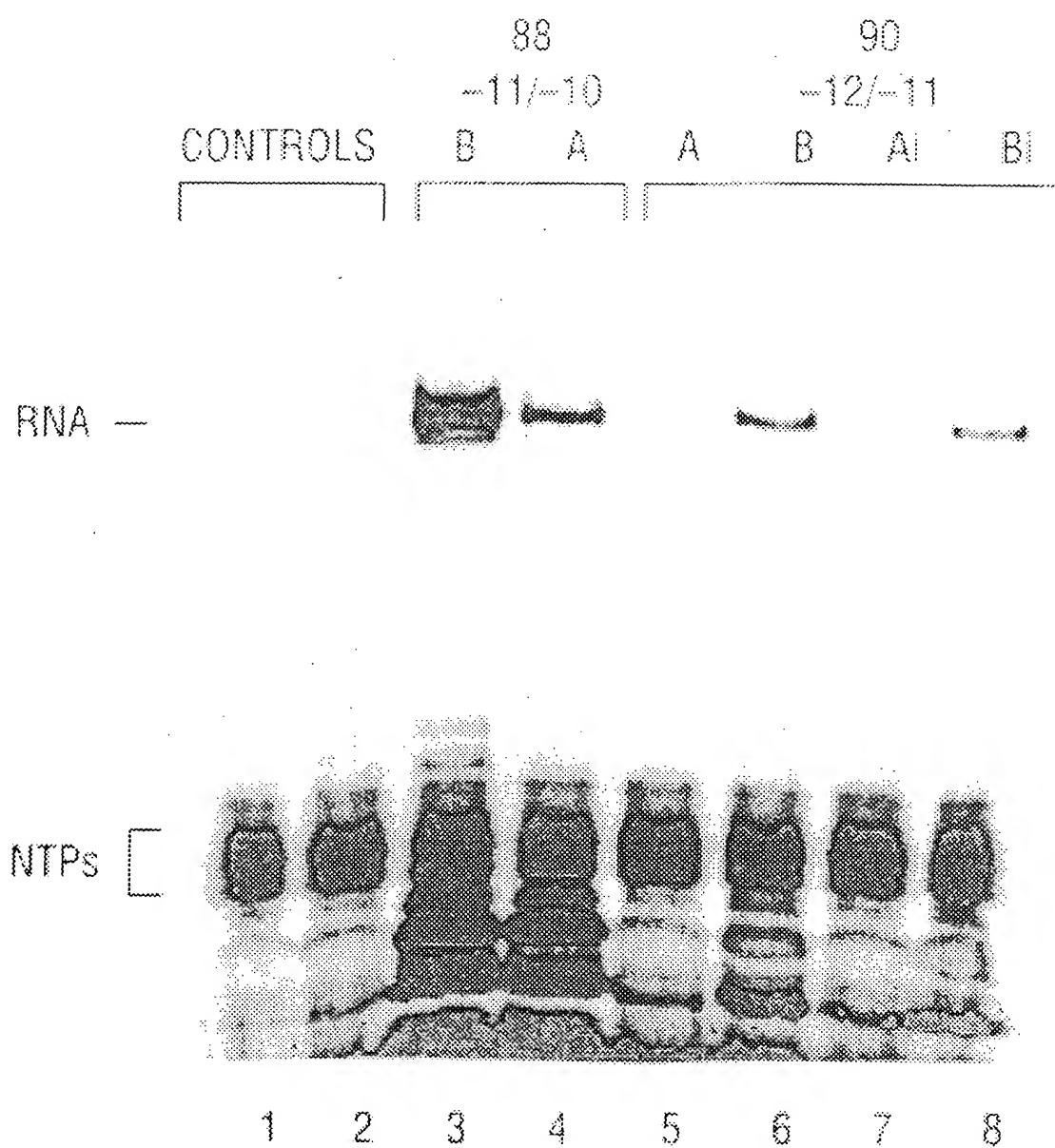


FIG. 91

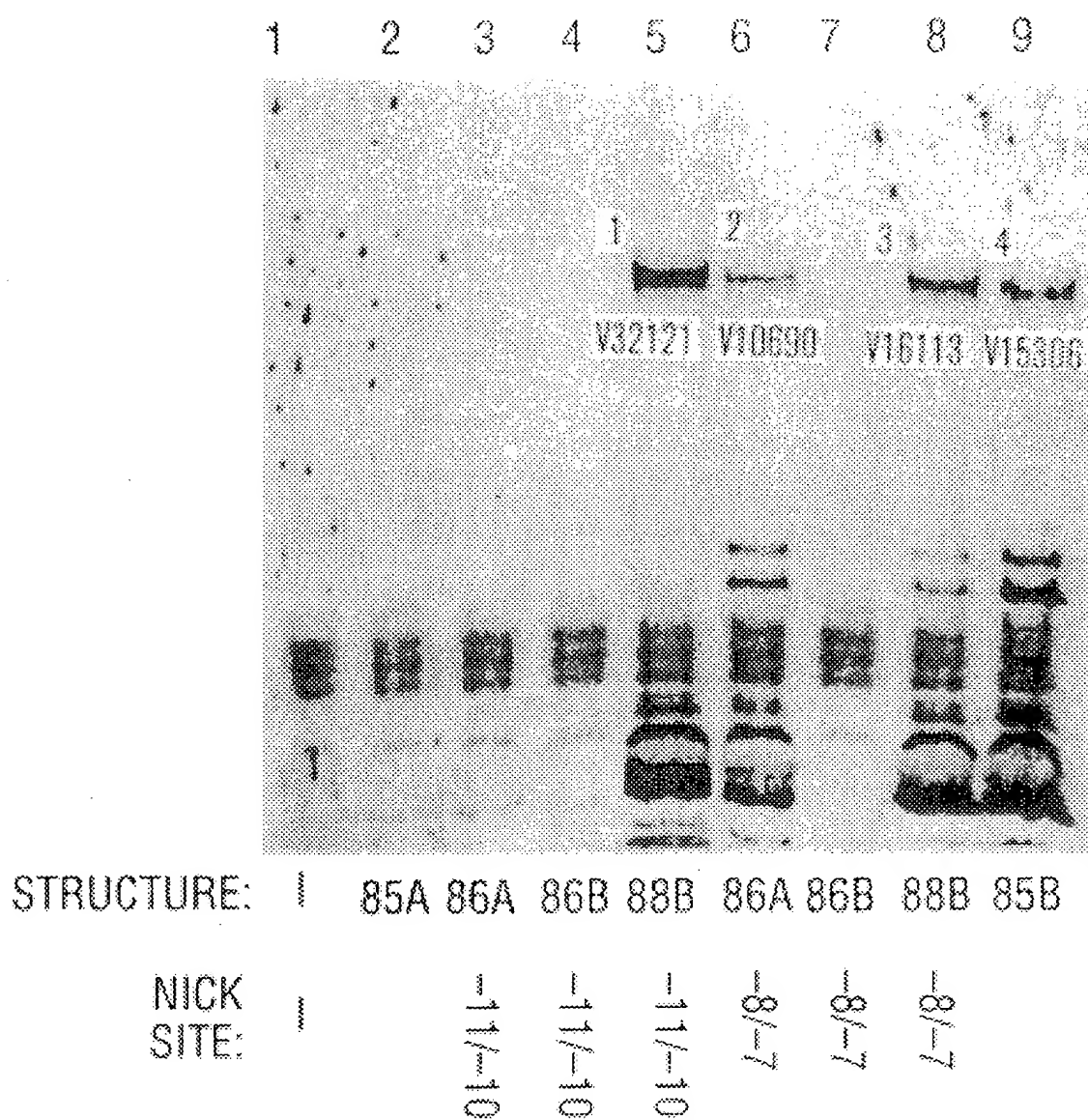


FIG. 92

1 3'-gctttaattatgctgagtgatatacccagaagataacctccagtttttgt-5'
 | | | | |
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

FIG. 93A

2 5'-cgaaattaatacgactcactata-3'
 3 3'-gctttaattatgctgagtgatatacccagaagataacctccagtttttgt-5'
 | | | | |
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

FIG. 93B

#073-065
 3 5'-cgaaattaatacgactcactatacccagaa-3'
 3 3'-gctttaattatgctgagtgatatacccagaagataacctccagtttttgt-5'
 | | | | |
 -23 -20 -15 -10 -5 -1
 | T7 promoter region |

FIG. 93C

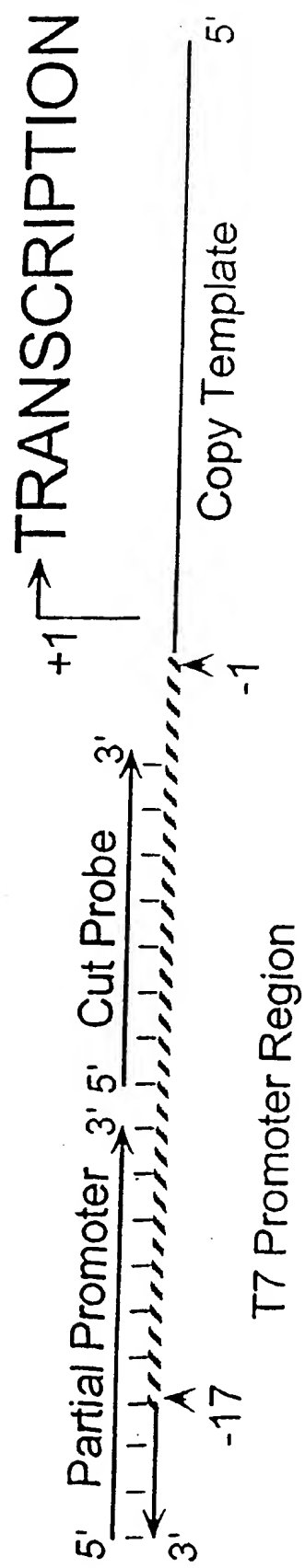
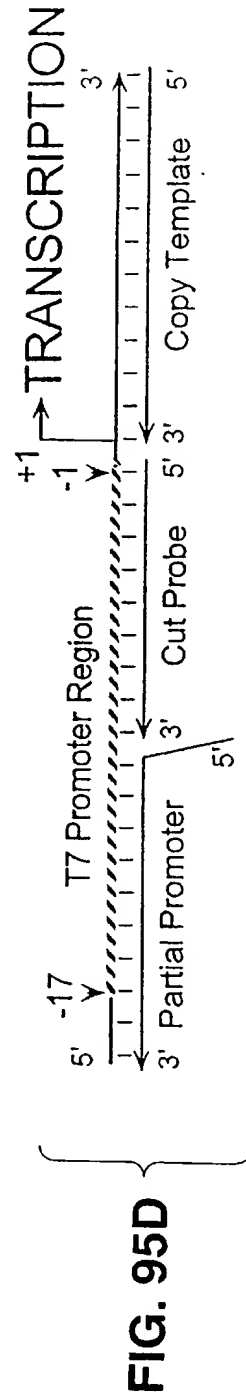
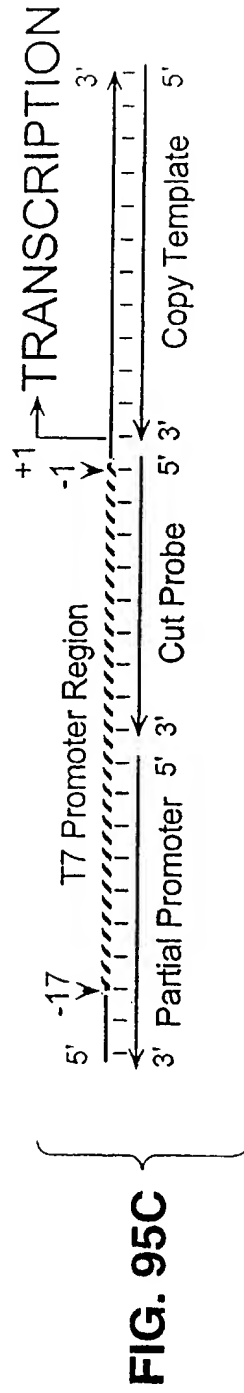
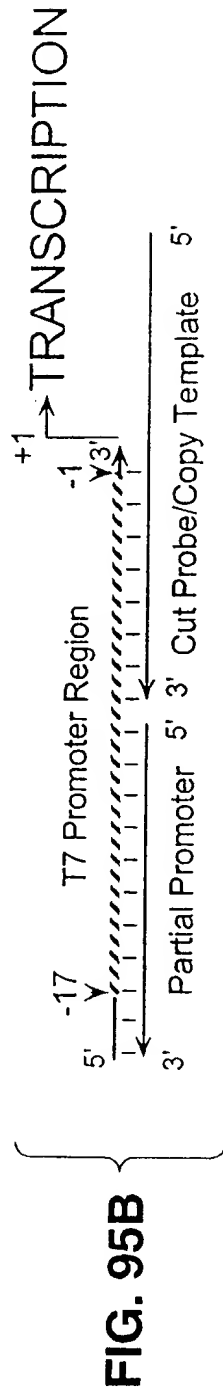
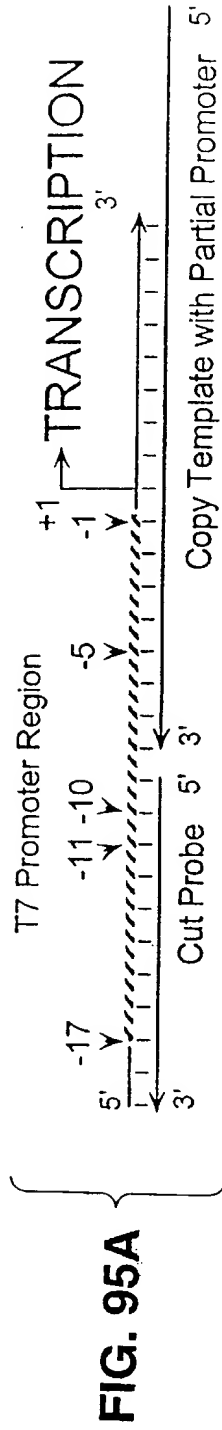


FIG. 94



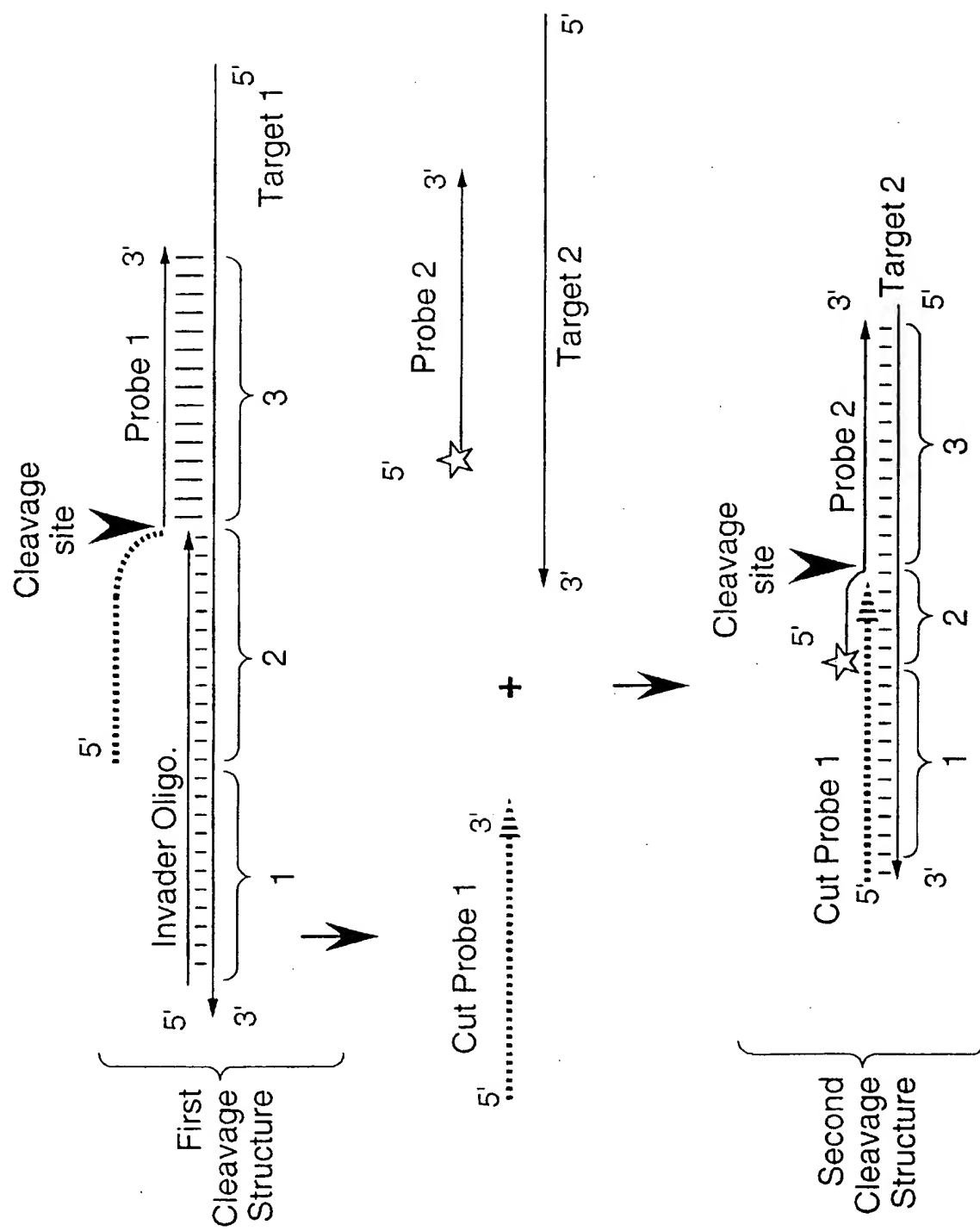


FIG. 96

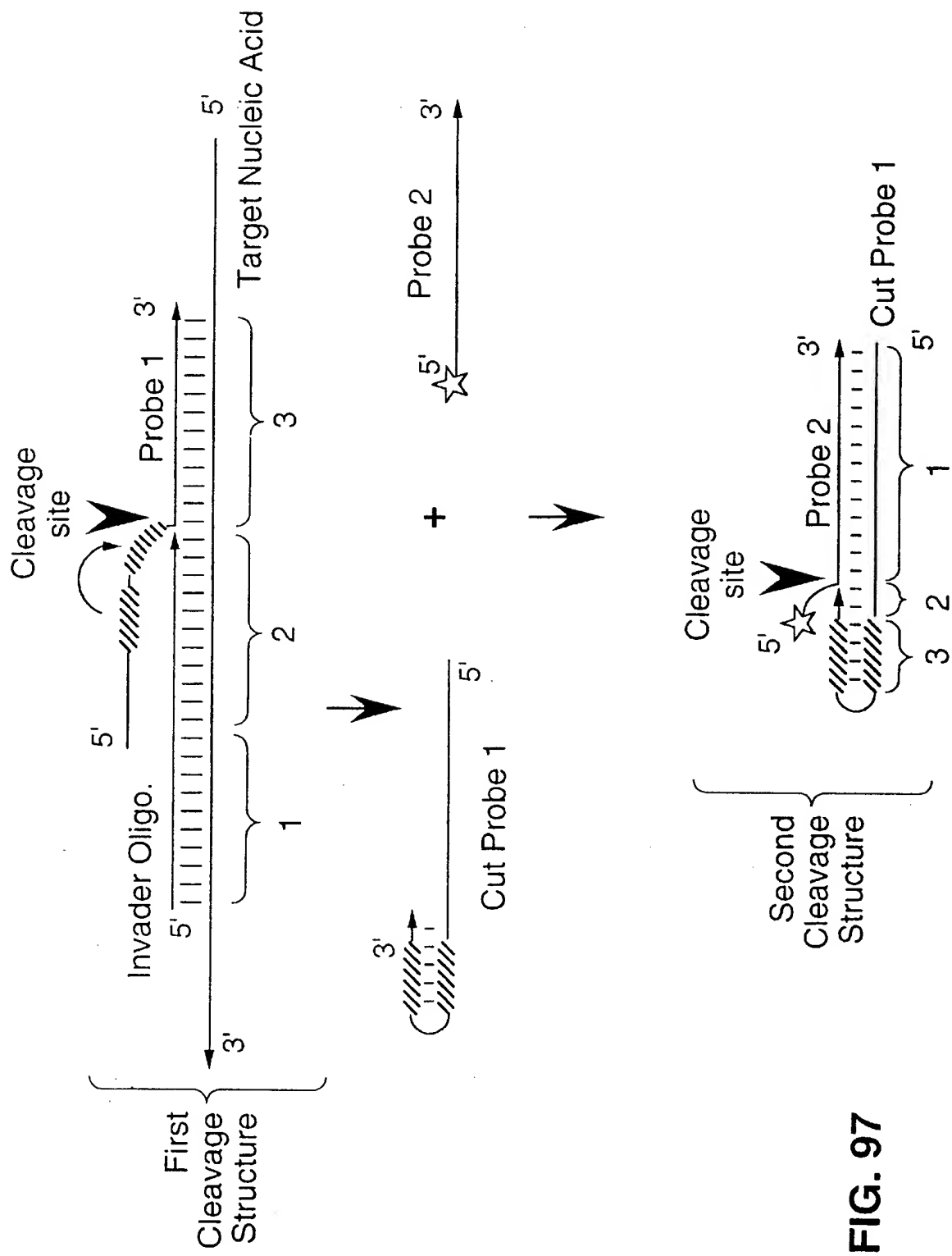


FIG. 97

PR1 probe

Cleavage site

5'FITT^TTCAGAGCCTAAT^G3'

IT3 Invader-Target

A^AACGAGCGTCTTT^G3'
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A^AAGCGTCTT^G3'
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A^ACGTCTT^G3'
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A^ATCTT^G3'
G AGAAGGTCTCGGATTAATTTTTTTTT5'

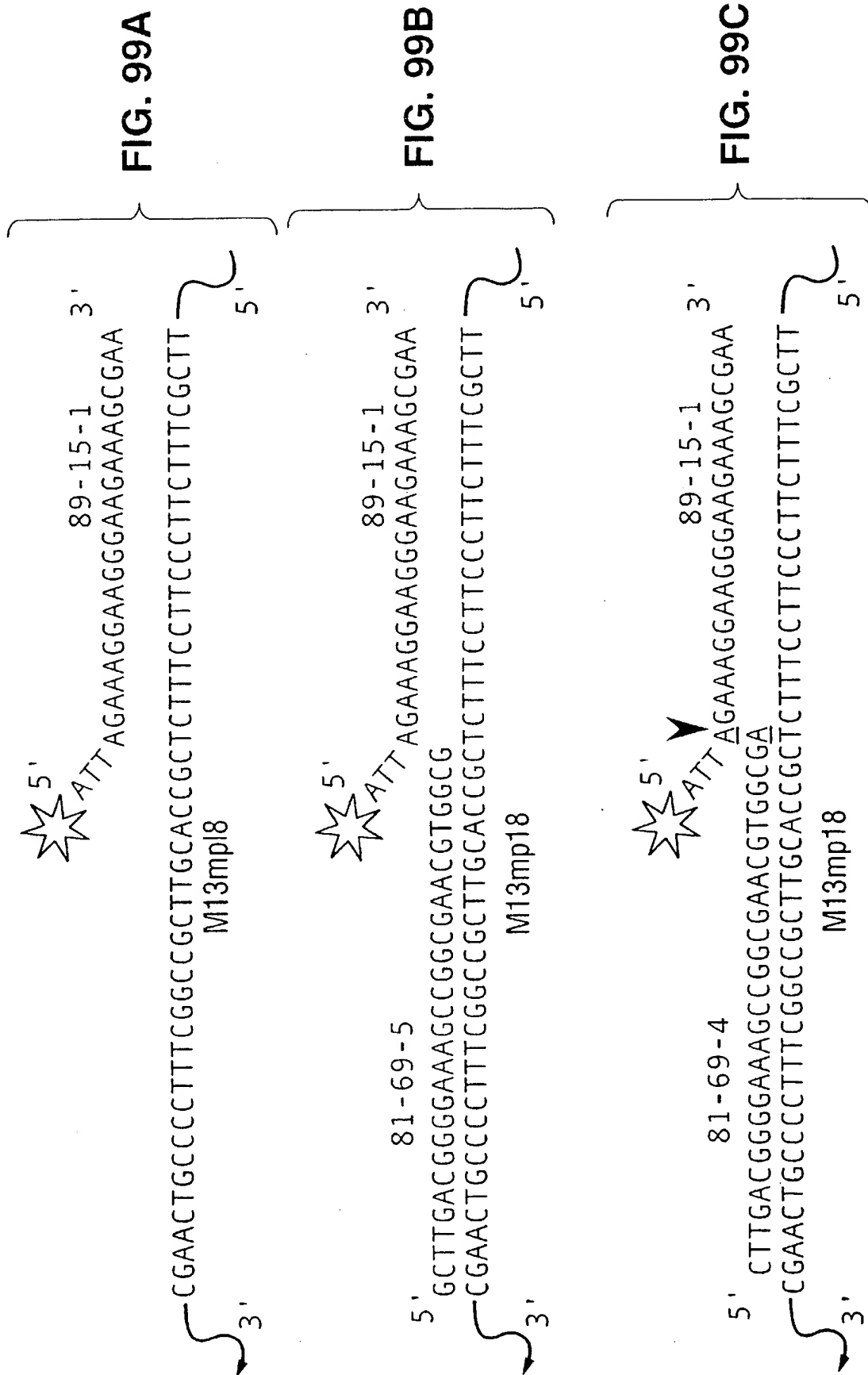
IT3-3 Invader-Target

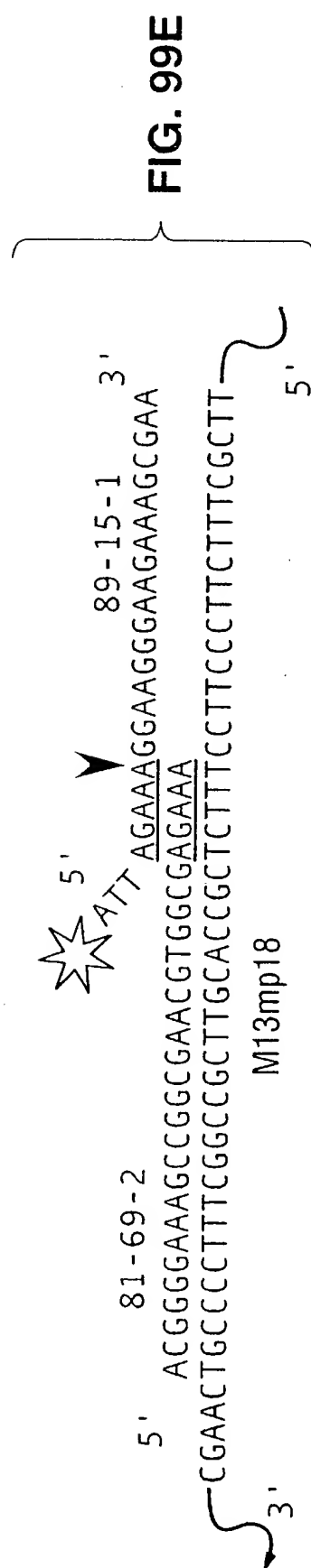
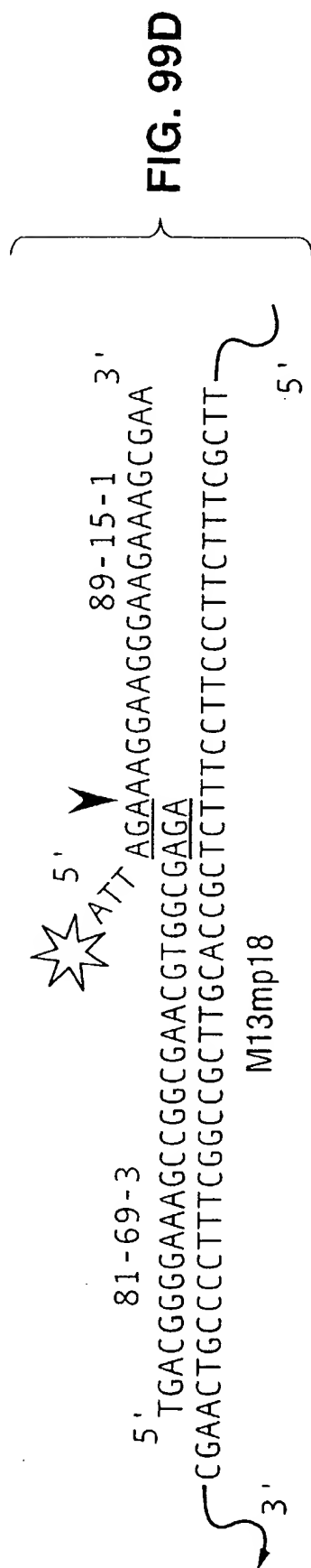
A^ACTT^G3'
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

FIG. 98





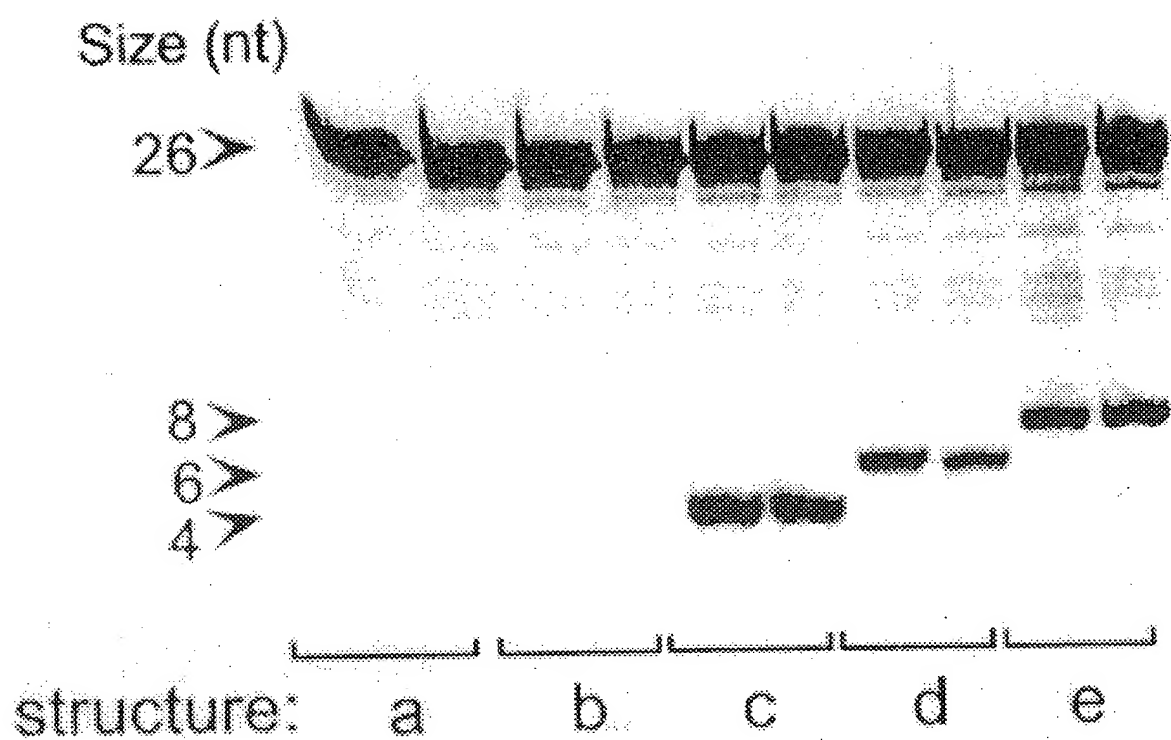


FIG. 100

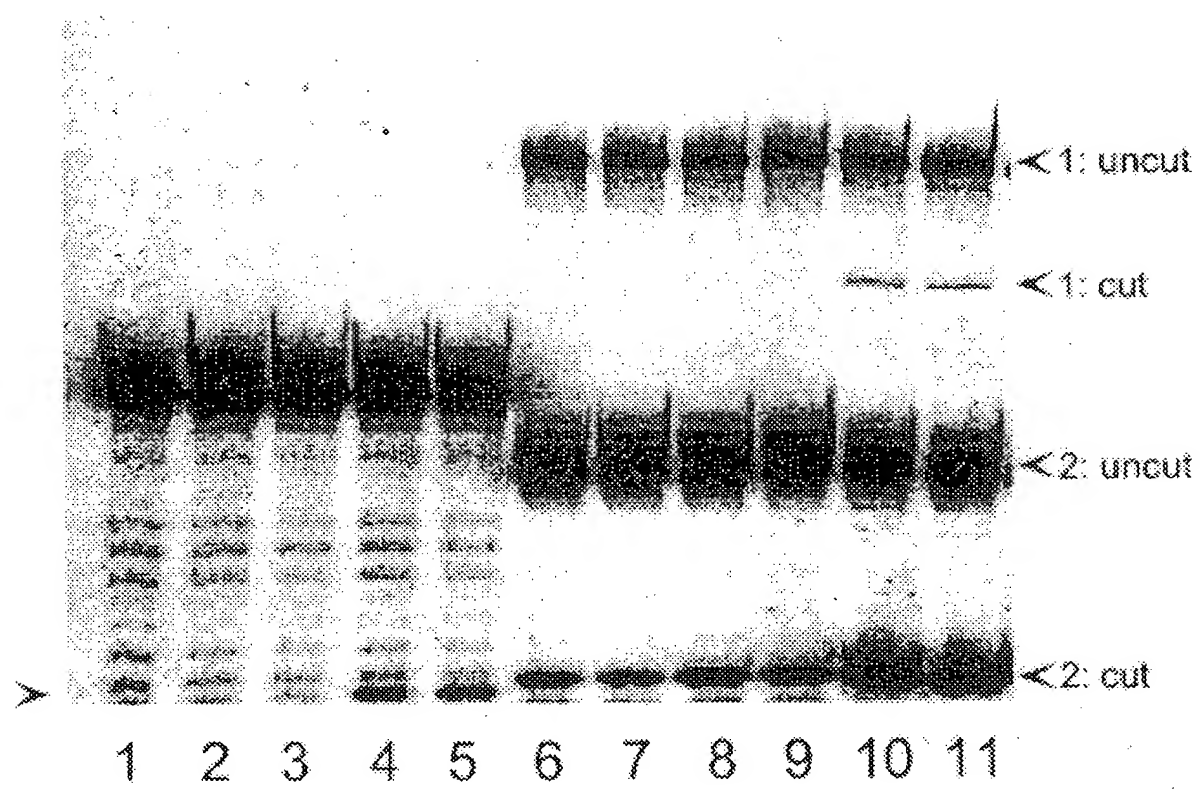
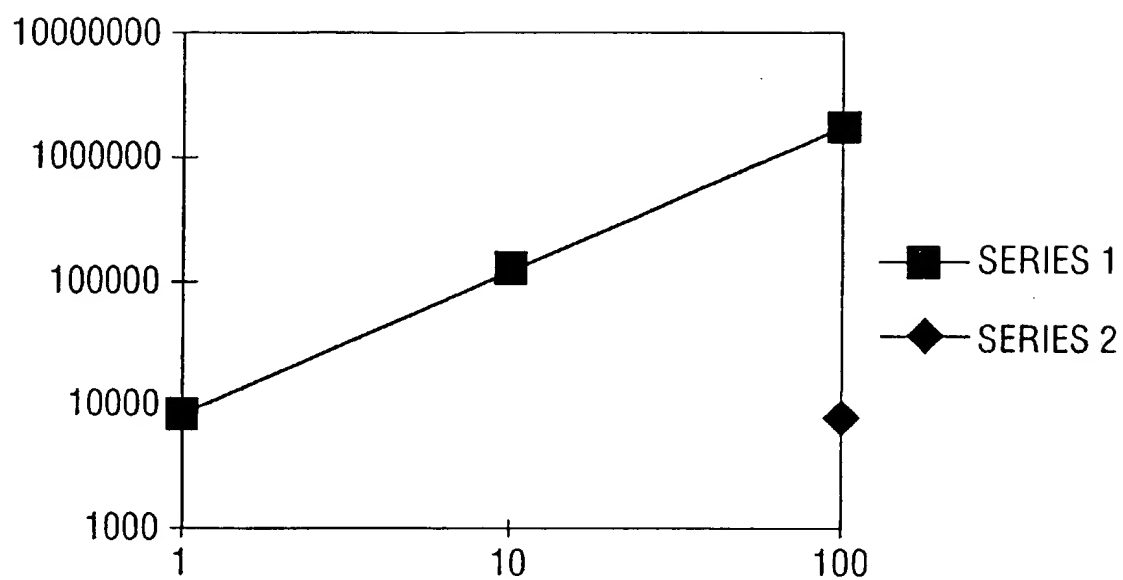


FIG. 101A



attomoles/target	basic invader	invader sqrd
1		8386
10		133185
100	8512	1862211

FIG. 101B

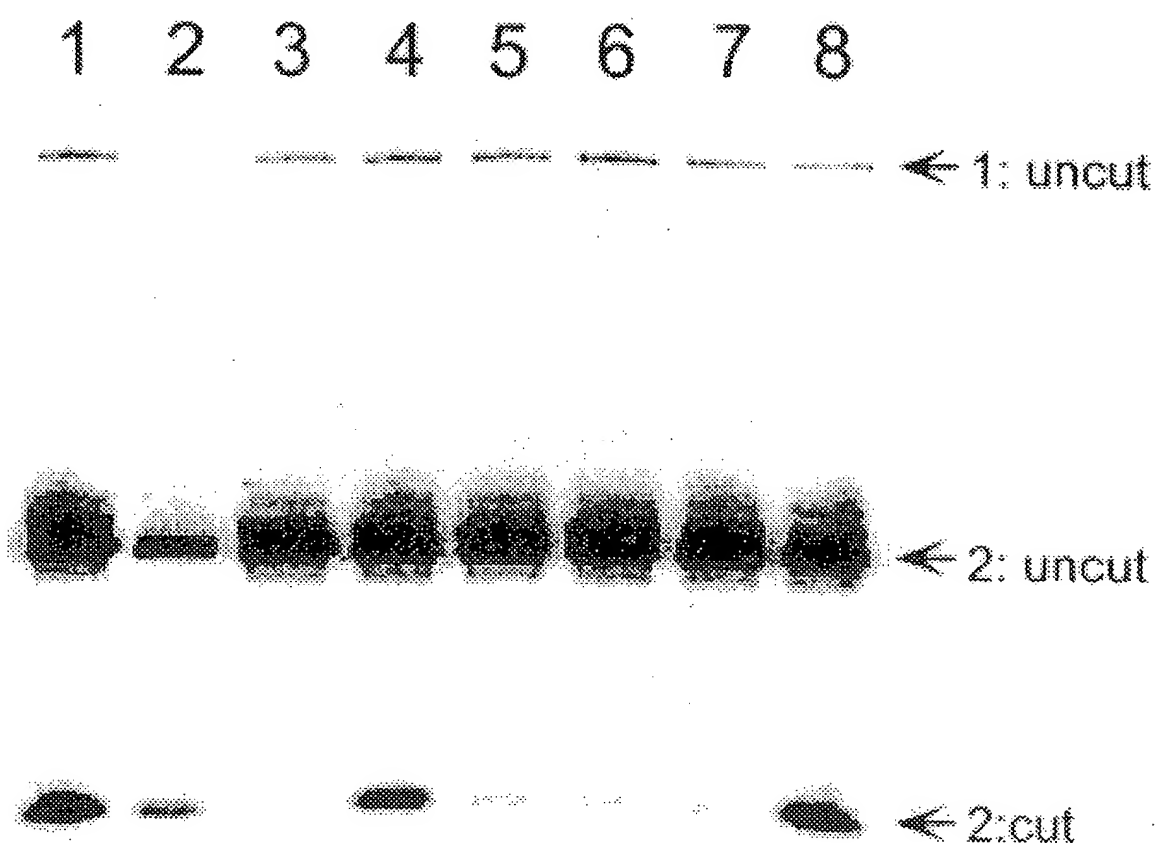


FIG. 102

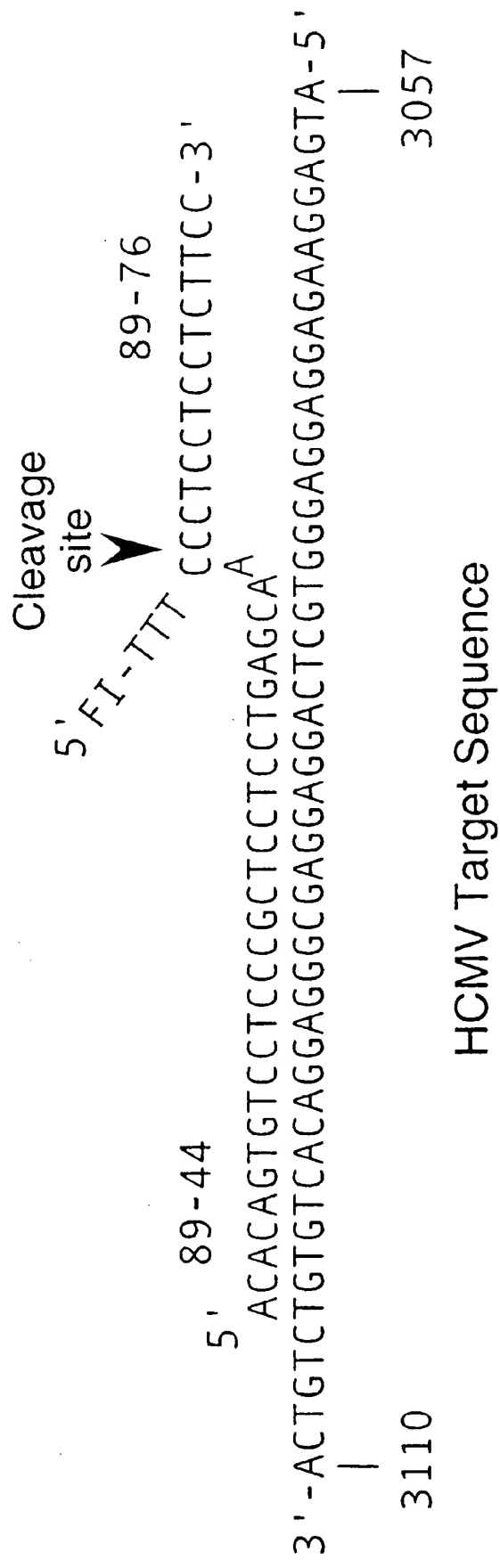


FIG. 103

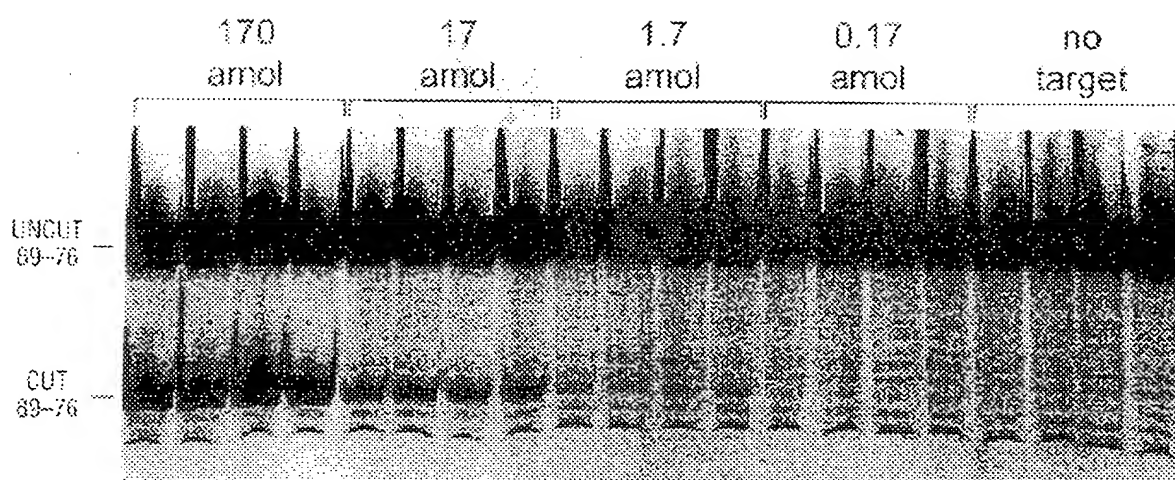
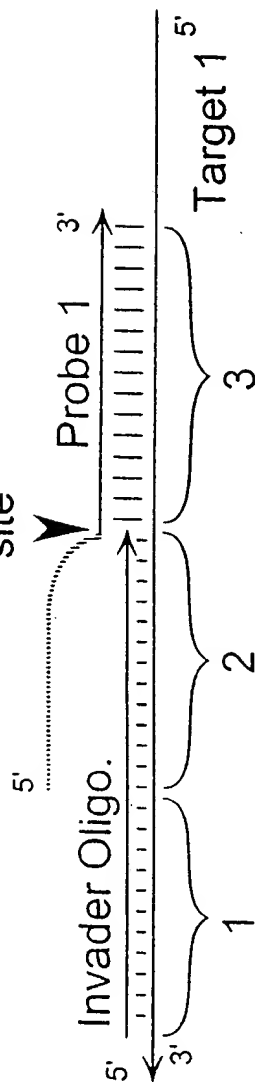


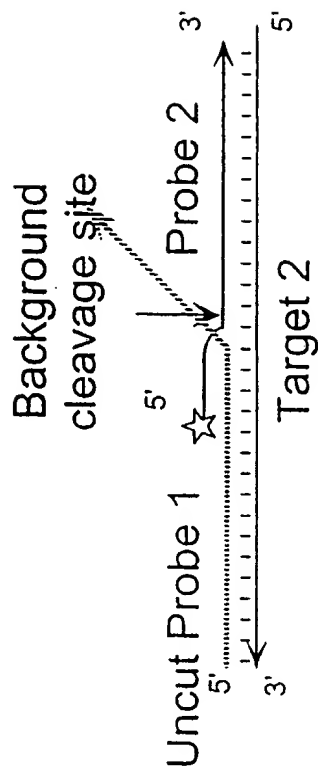
FIG. 104

FIGURE 105

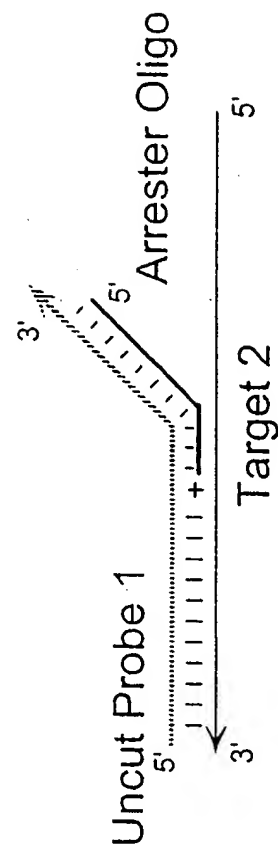
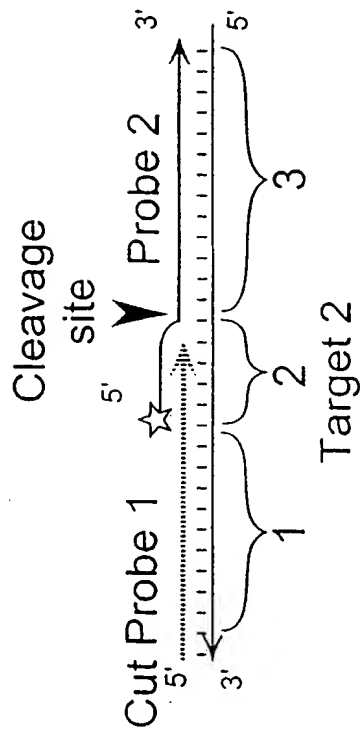
Cleavage site



1



2a



2b

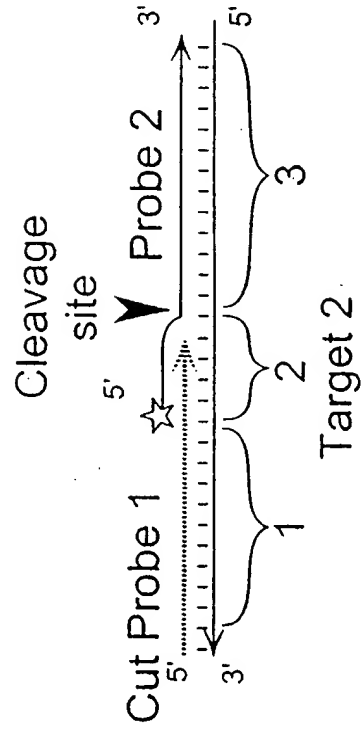


FIGURE 106

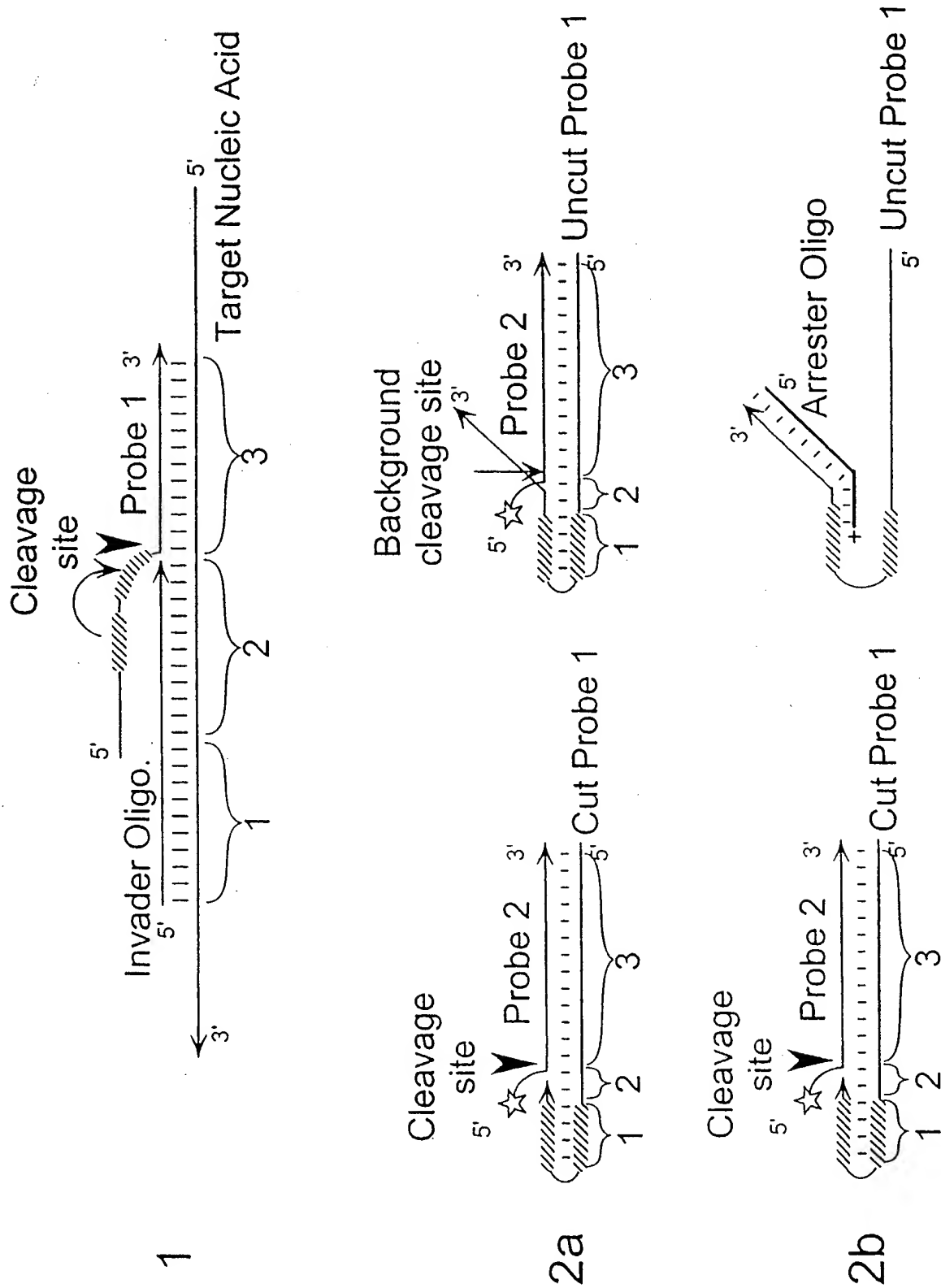
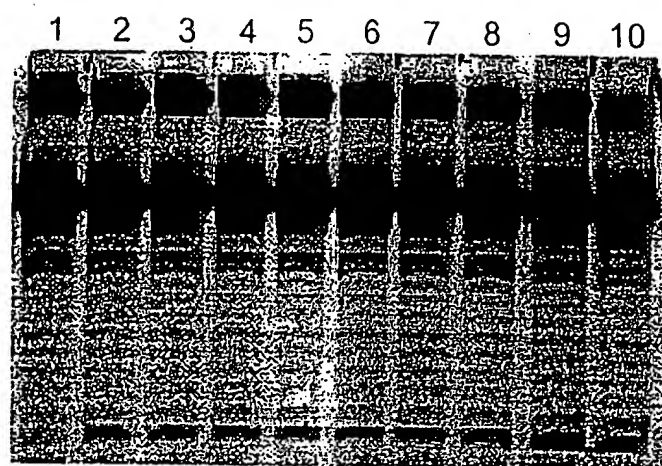
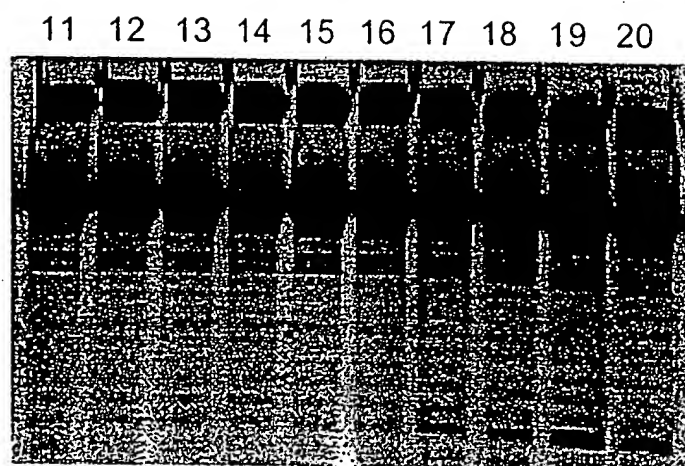


FIGURE 107

A



B



C

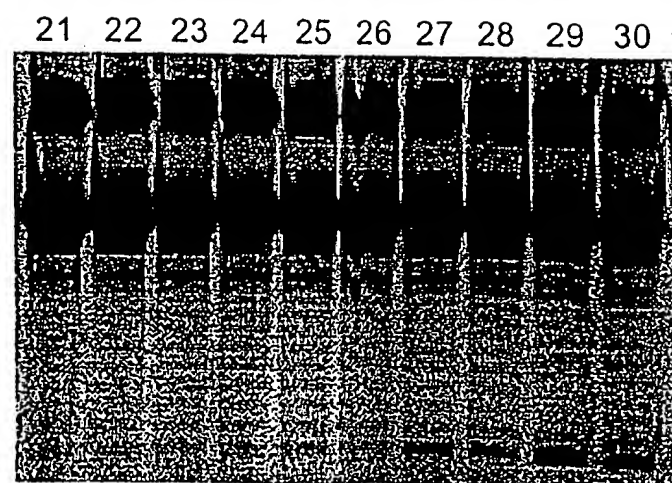


FIGURE 108A

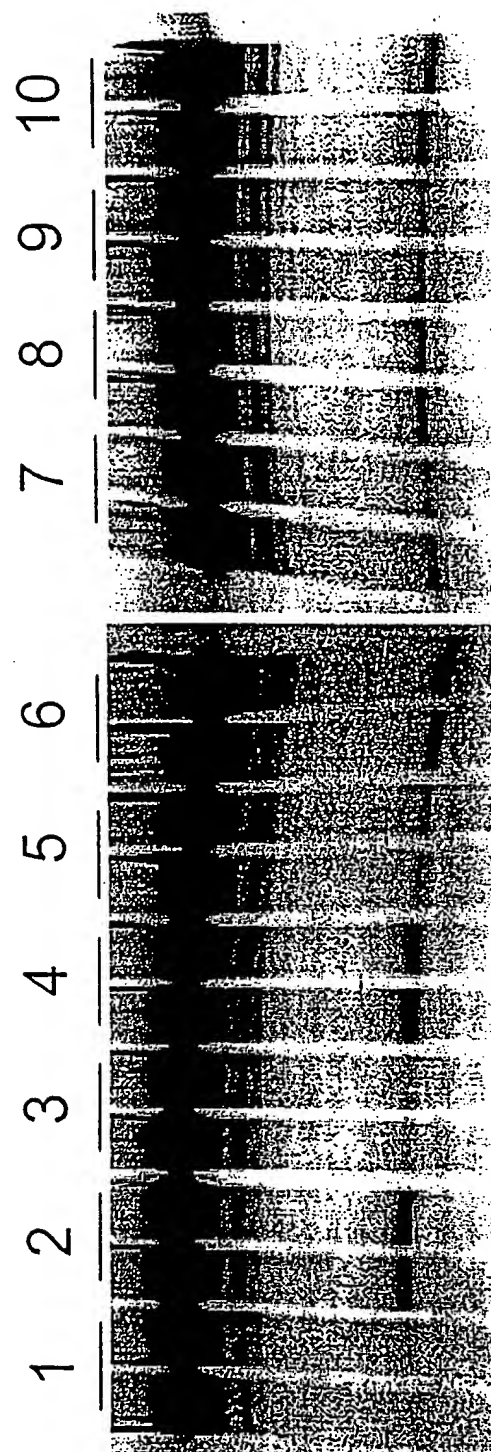


FIGURE 108B

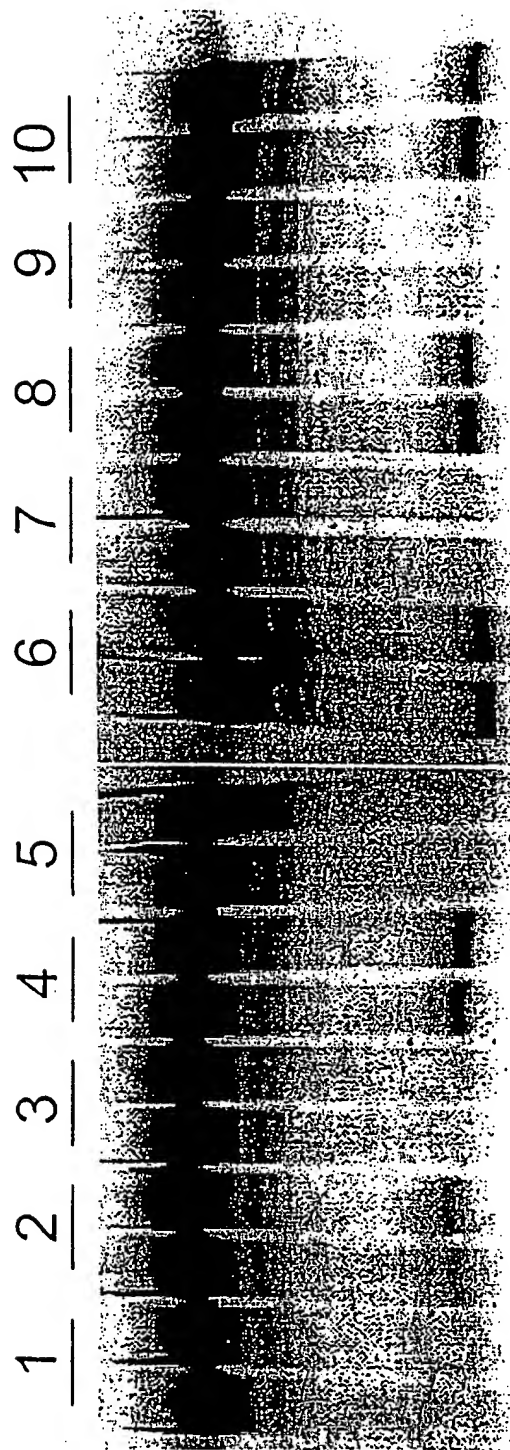
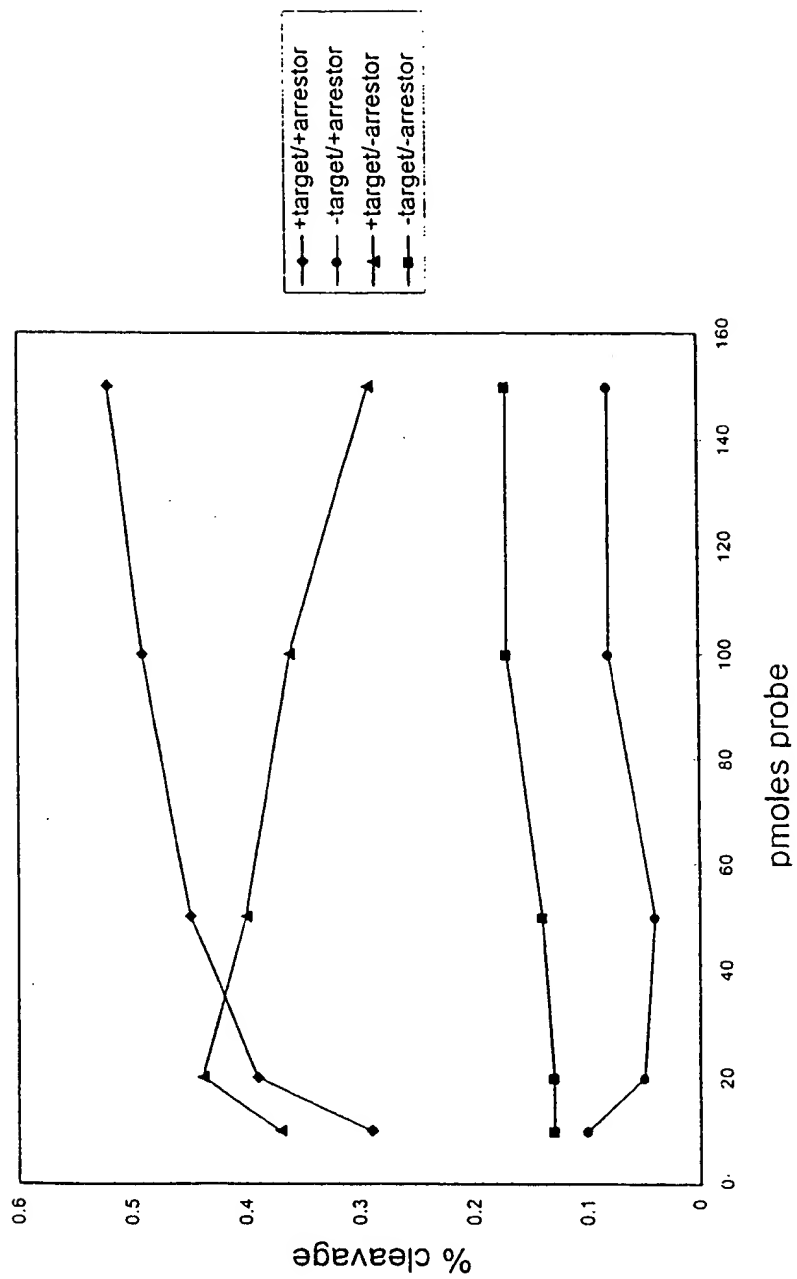


FIGURE 108C



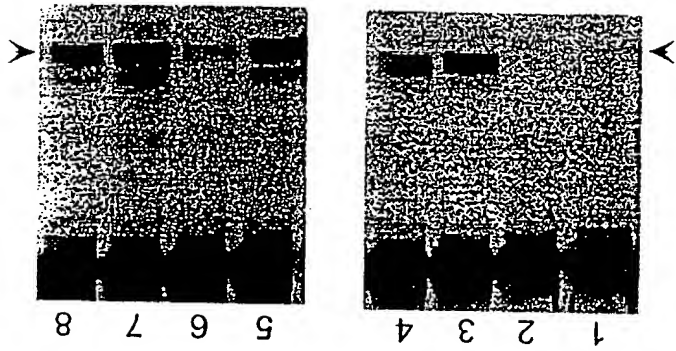


FIGURE 109A

FIGURE 109B

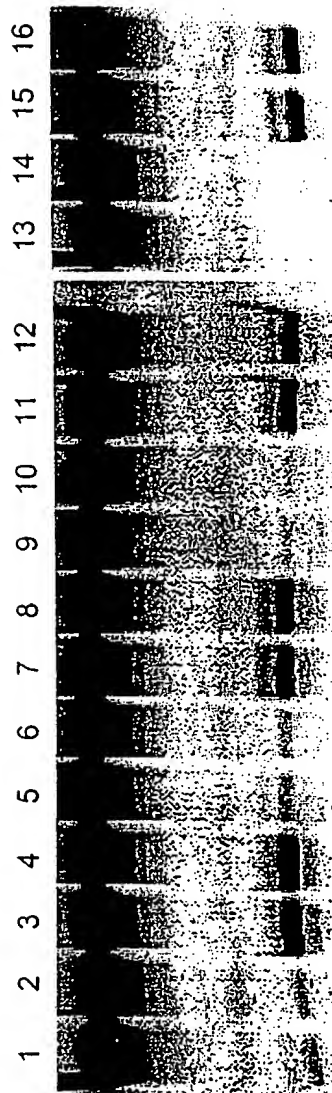


FIGURE 110A

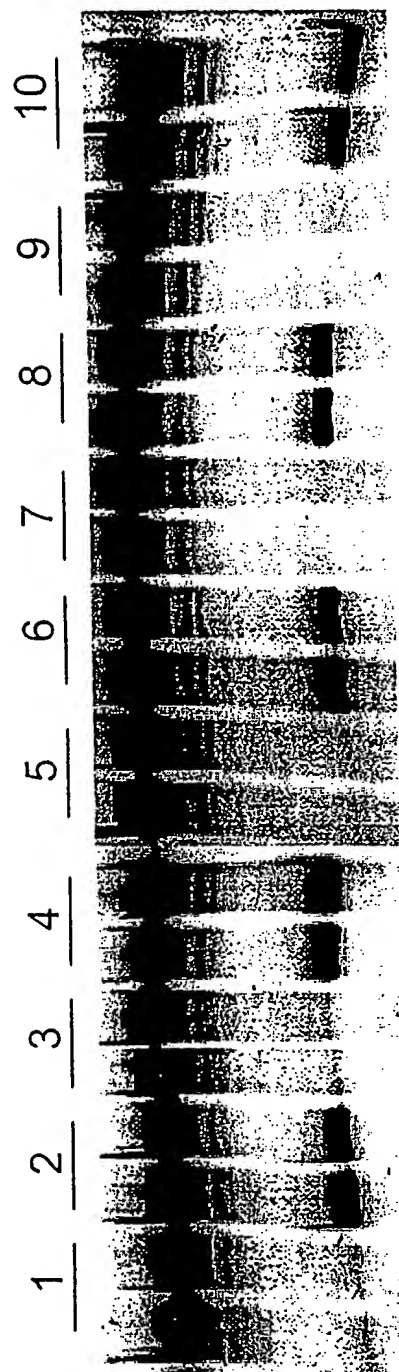


FIGURE 110B

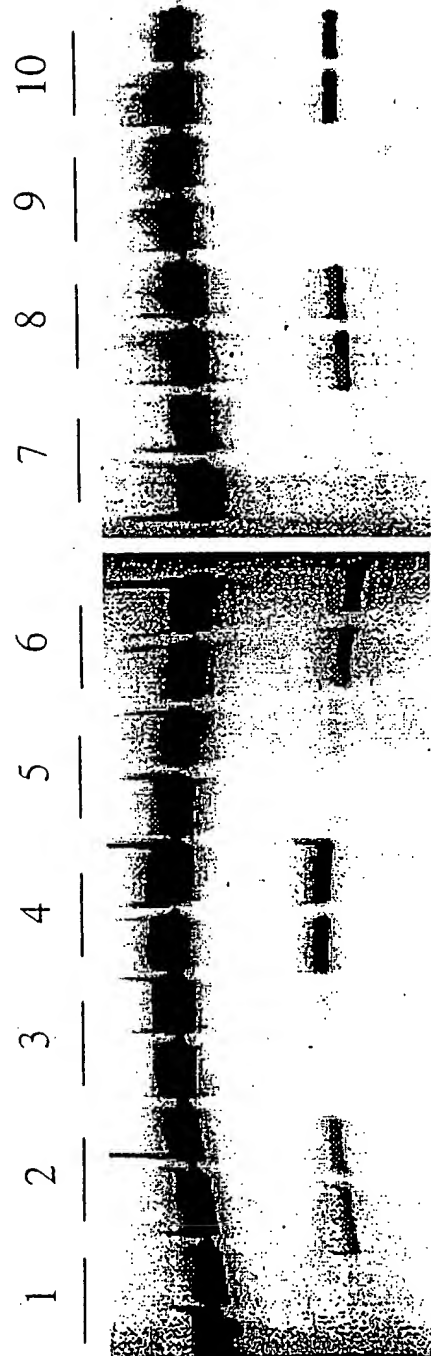


FIGURE 110C

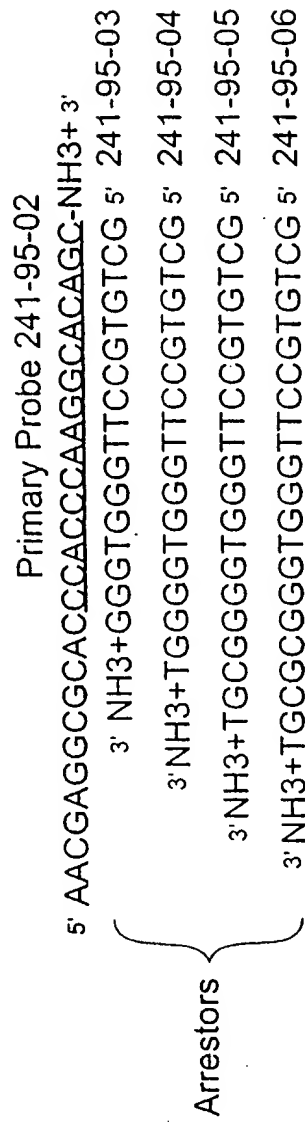


FIGURE 111

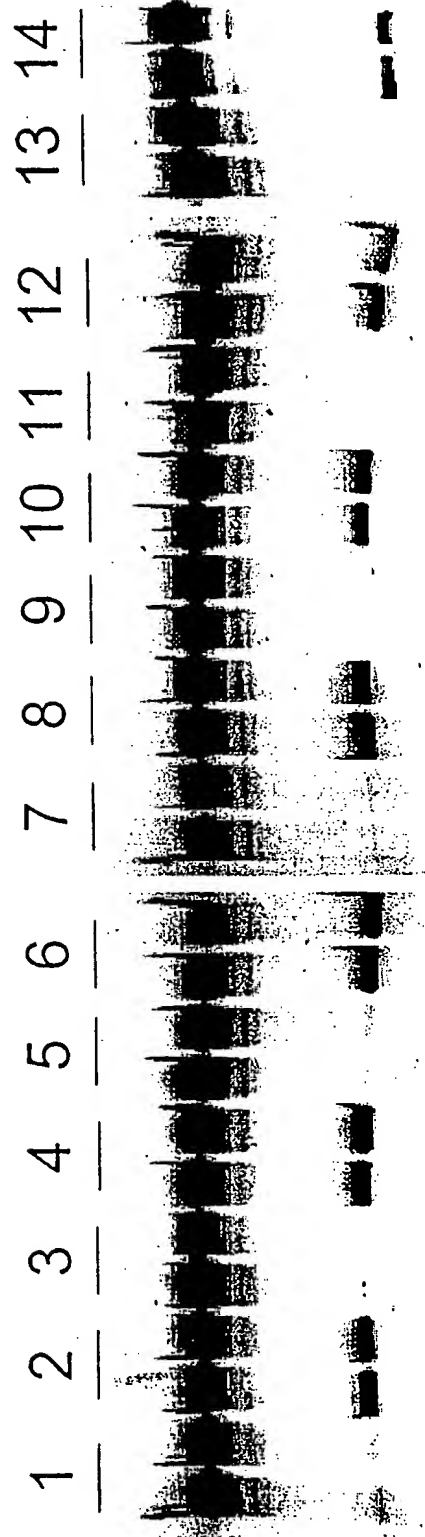


FIGURE 112

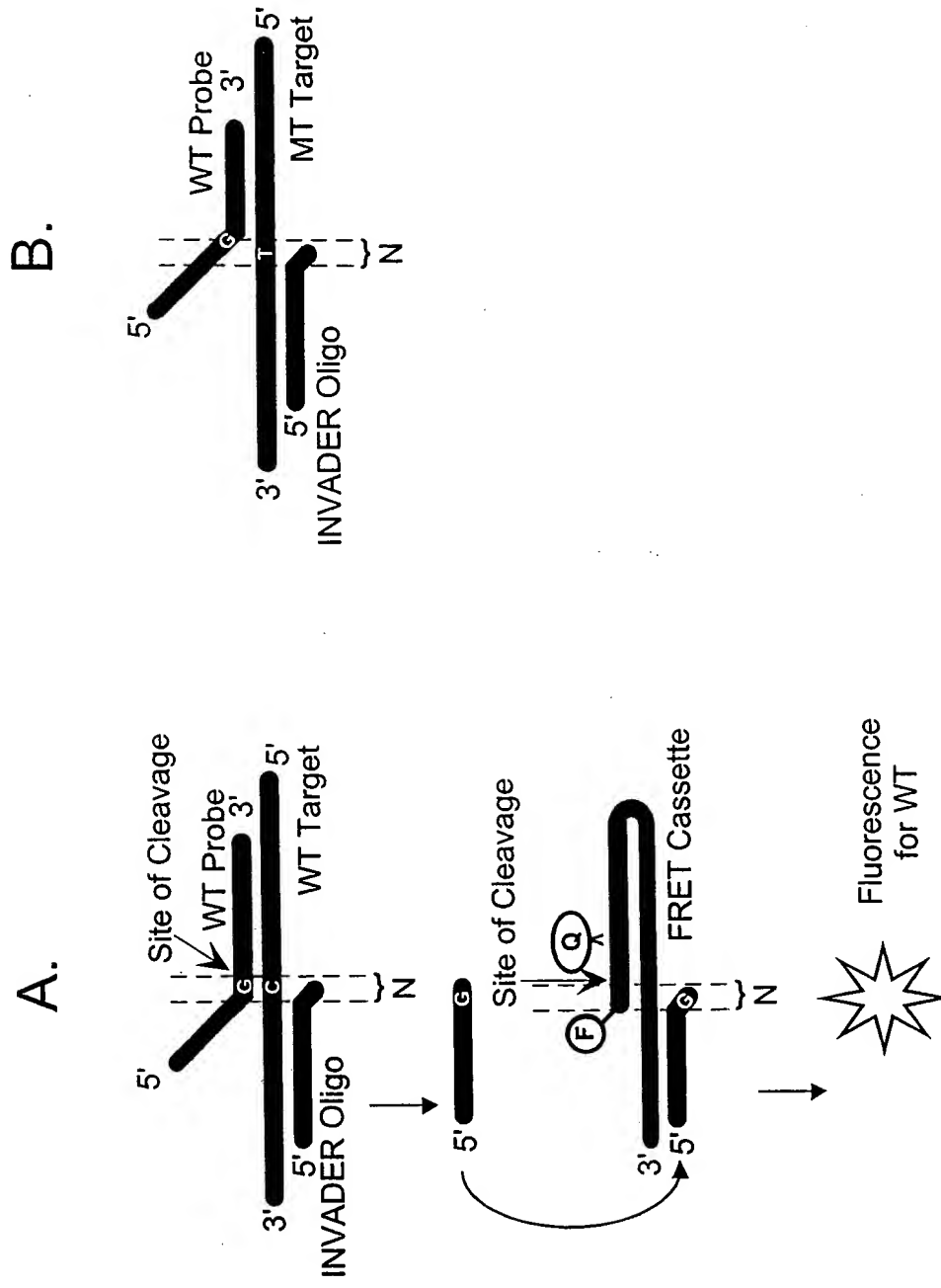


FIGURE 113A

5'-AACGAGGCGCAAGCAGTCCTCCATGT
 5'-CGGTACTGCACGAGGCGCCGCT
 3'-GAGCGGCGCCATGACGTGGTCCGCGCGGTGCAGGAGGTACAGGCGCGGGTC-5'

(F) (Cy3)
 CCTCGTCTCGGT T
 AACGAGGCGCACG
 3'-CTTCTCCGCGTGGGAGCAGAGCCT T

FIGURE 113B

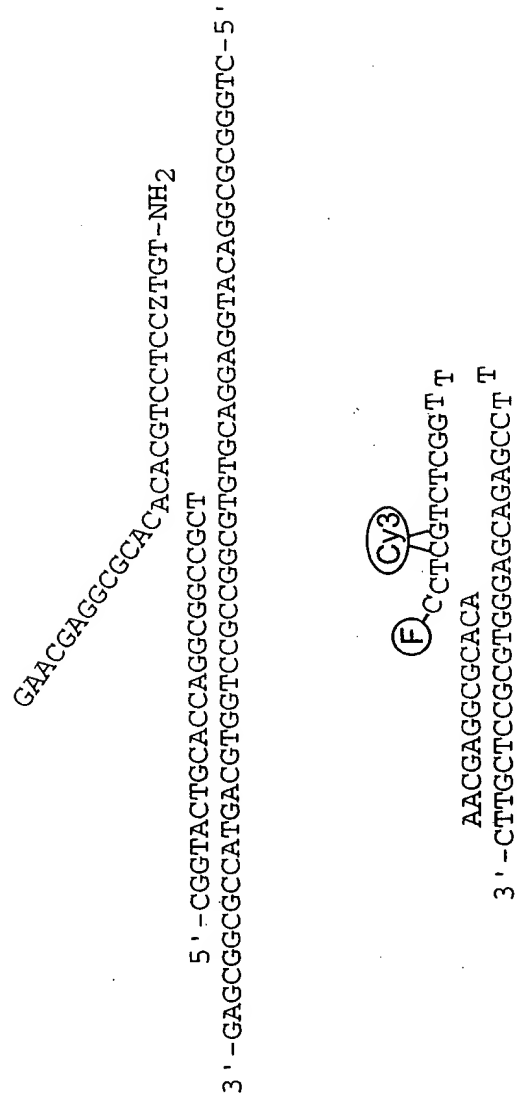


FIGURE 113C

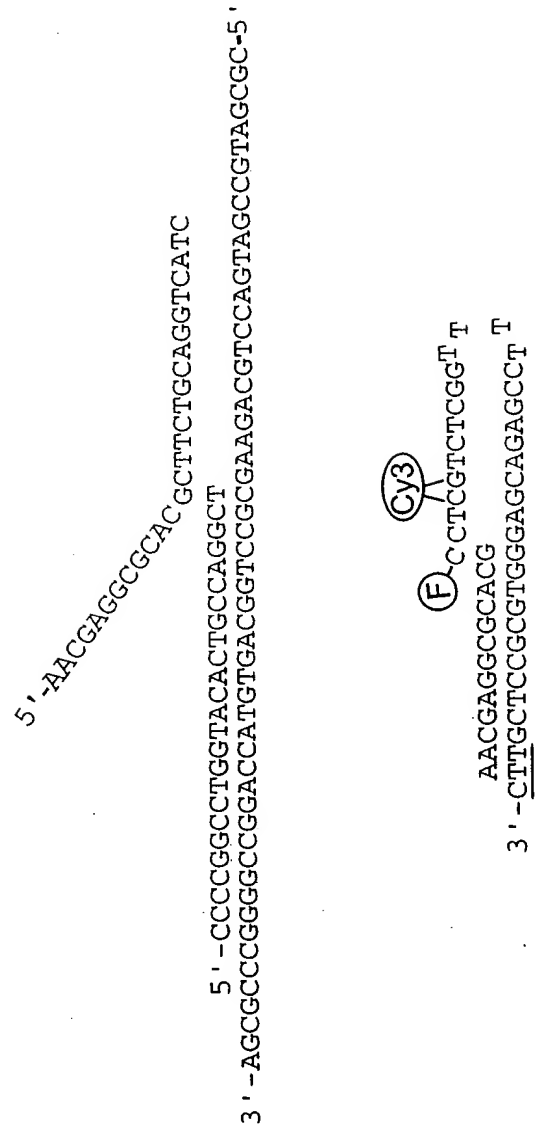


FIGURE 113D

5'-AACGAGGCGCACTTCTGCZGGTCATC
 5'-CCCCGGCCTGGTACACTGCCAGGCT
 3'-AGCGCCCGGGCCGACCATGTGACGGTCCGTGAAGACGTCCAGTAGCCGTAGCGC-5'

AACGAGGCGCACA
 3'-CTTGCTCCGCGTGGGAGCAGAGCCT T
 (F) CCTCGTCTCGG^T T
 (Cy3)

FIGURE 114A

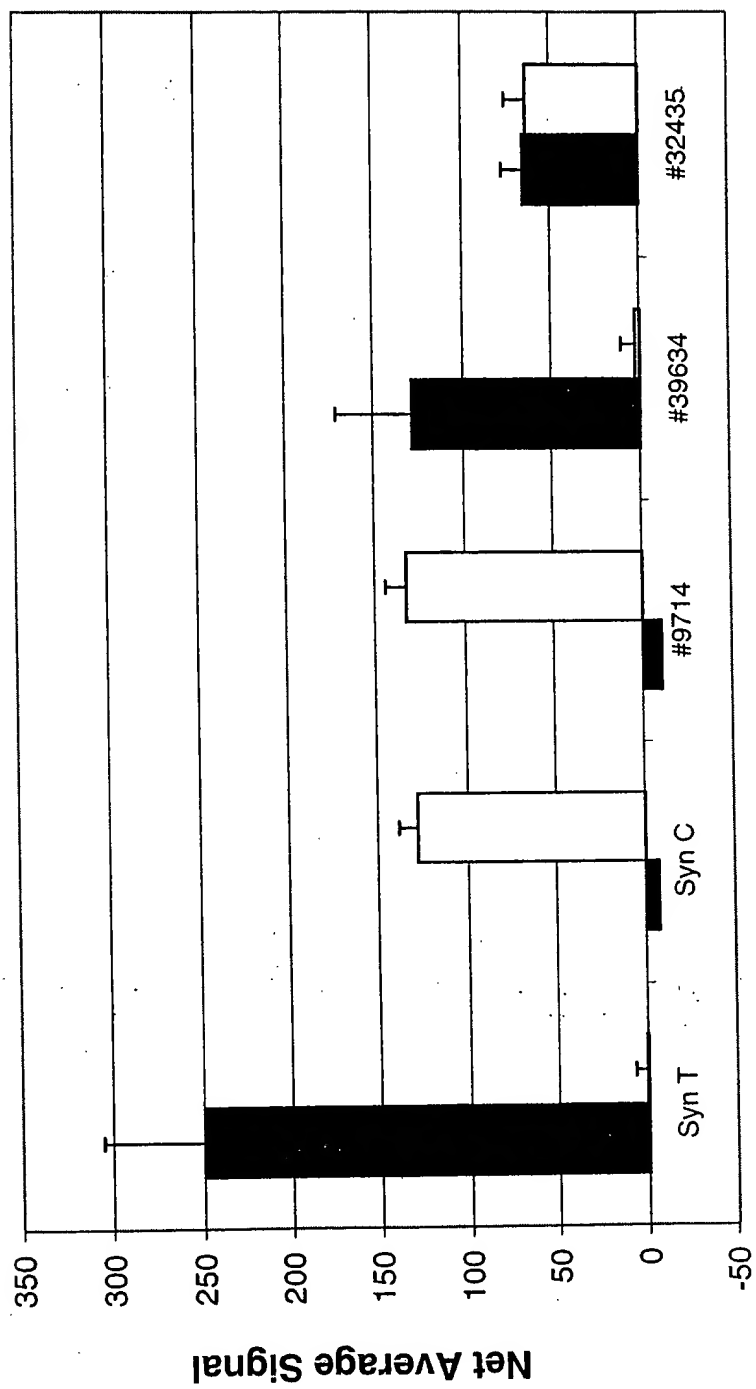


FIGURE 114B

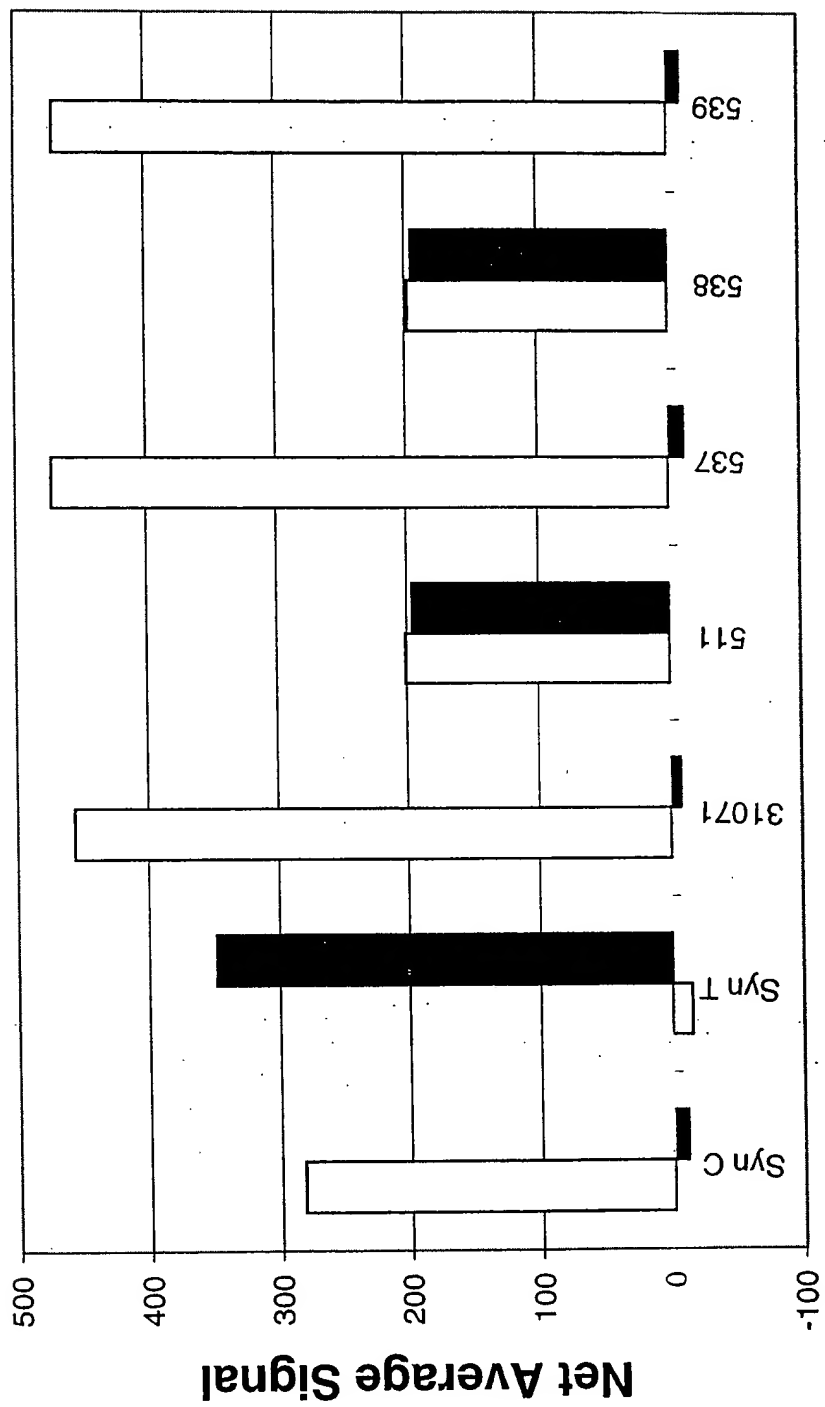
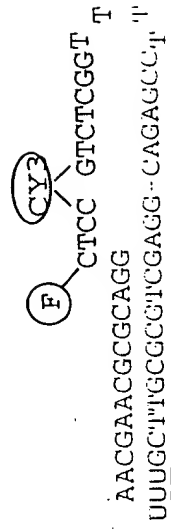


FIGURE 115A

5'-AACGAACGGCAGGCCAGGTGGAGCATT-3'
 5'-CCCCCTGGGGAAGAGCAGAGATATACGTC
 3'-GACCCCTTCTCGTCTCTATATGCACGGTCCACCTCGTGG-5'



 AACGAACGGCAGG

UUUGCTTCGAGG-CAGAGCC

FIGURE 115B

5'-AACGAACGCGCAGACCAGGTGGAGCAC-3'
5'-CCCCTGGGGAAGAGCAGAGATATACGTC
3'-GACCCCTTCTCGTCTCTATATGCATGGTCCACCCTCGTGG-5'

(F) (CY3) CTCC GTCTCGG^T
AACGAACGCGCAGA
UUUGCTTGGCGGTCGAGG-CAGAGCC^T

FIGURE 115C

5'-AAGCAGCAGCACGATCATAGAACACGAACAGTTT-3'
 5'-GGGCTCCACACGCGGACTCTCATTT
 3'-GCCCCGAGGTGTGCCGTGAGAGTACTAGTATCTTGTGCTTGTCTCGA-5'

AAGCAGCAGCAGC
 UUUCGTGCGTGTGCG-CAGAGCCCT
 (F) ACGC GTC TCCGCT T
 (CY3)

FIGURE 115D

5'-AAGCAGCAGCACCATCATAGAACACGAGTTT-3'
5'-GGGCTCCACACGGCGACTCTCATT
3'-GCCCCGAGGTGTGCCGCTGAGAGTAGTAGTATCTTGTGCTTGTCTCGA-5'

Ⓕ ACGC GTCTCGG T
AAGCAGCAGCAC
UUUCGTGCGTCGTGCG-CAGAGCC T

FIGURE 116

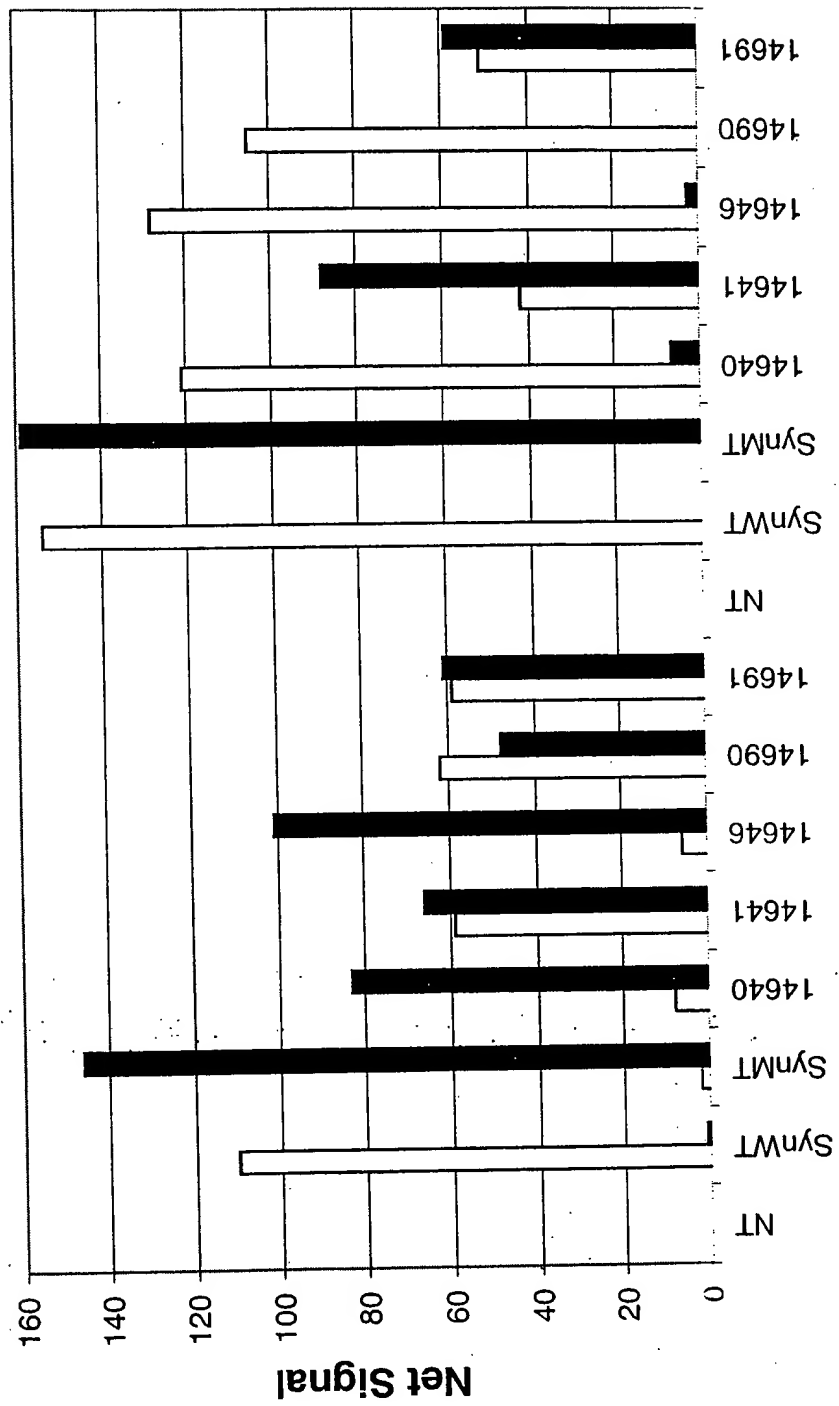


FIGURE 117A

5'-AACGAGGCGCACGCTCCCGCAGACAC-3'
 5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC
 3'-GGAGTTTCTTTTCGACGCACACTACTTTAGCCGAGGGCGTCTGTGGAAG-5'

5'-AACGAGGCGCACGCTCGTCTCGGT^T
 3'-NH₂-TTTGCTCCGCGTGGGAGCAGAGCC^T

(F) (Cy3)

FIGURE 117B

5'-AACGAGGCGCACTCCCGCAGACACC-3'
 5'-CAAAGAAAAGCTGCGTGATGATGAAATCGC
 3'-GGAGTTTCTTTTCGACGCACTACTTTAGCTGAGGGCGTCTGTGGAAG-5'

5'-AACGAGGCGCACA
 3'-NH₂-TTTGCTCCCGCTGGGAGCAGAGCC-T
 (F) (CY3)

FIGURE 118

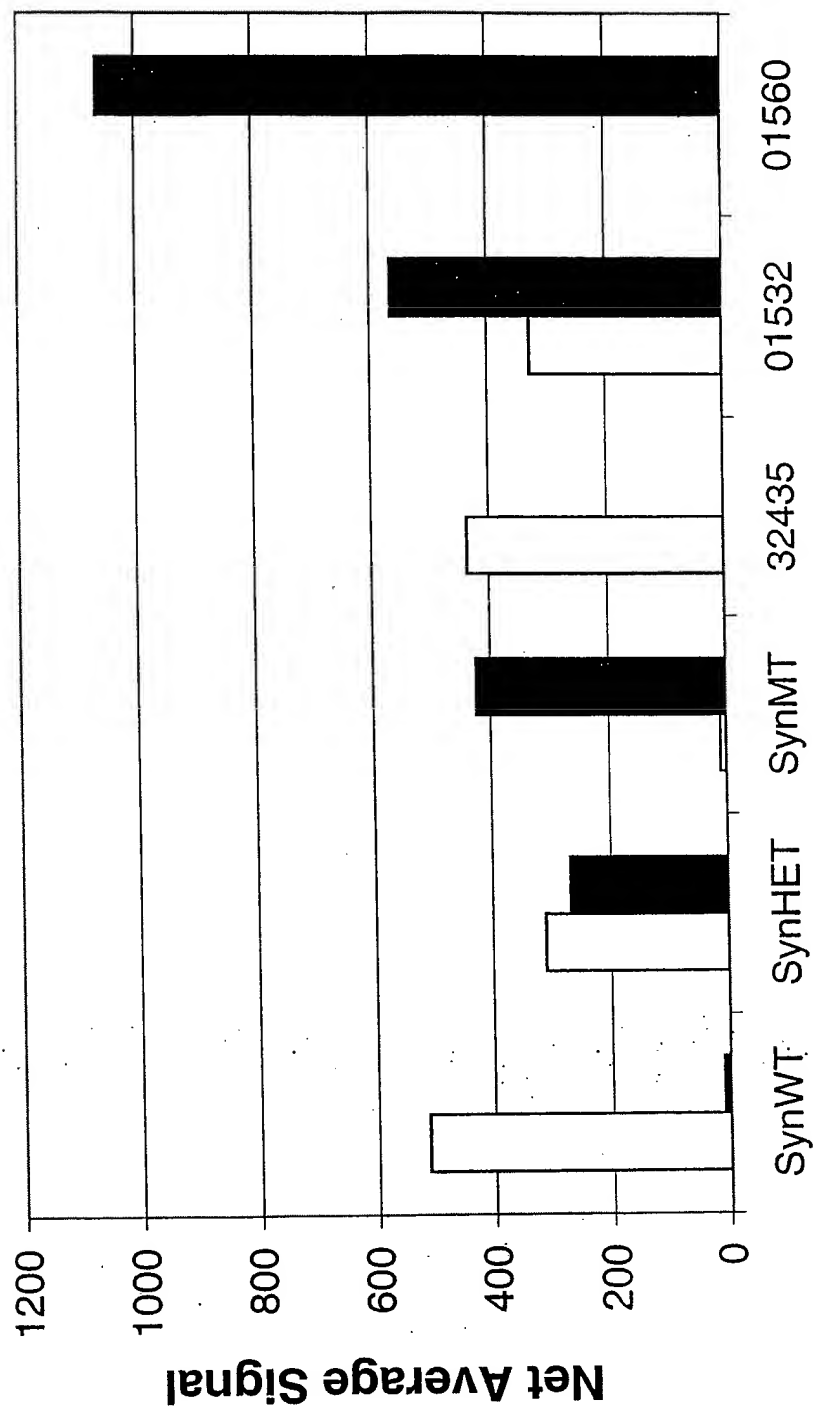


FIGURE 119A

5' - AACGAGGCGCAC GAGCCTCAATGCTCCC - NH₂ - 3'

5' - TATGGTTCCCAATAAAAGTGACTCTCAGCT

3' - TTGATACCAAGGGTTATTTTCACTGAGAGTCGCTCGGAGTTACGAGGGGTCA - 5'

5' - AACGAGGCGCACG

3' - NH₂ - TTTGCTCCGCGTGGGAGCAGAGCC - T

(F) (Cy3)

CCTCGTCTCGGT T

FIGURE 119B

5' - AACGAGGCGCAC AAGCCTCAATGCTCCC - NH₂ - 3'

5' - TATGGTCCCAATAAAAGTGACTCTCAGCT

3' - TTGATACCAAGGGTTATTTTCACTGAGAGTCGTTCTGGAGTTACGAGGGTCA - 5'

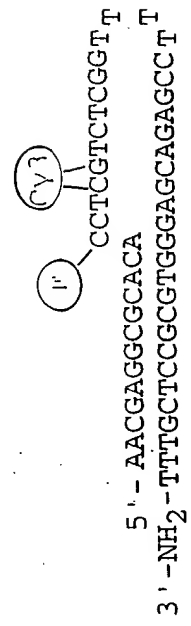


FIGURE 120

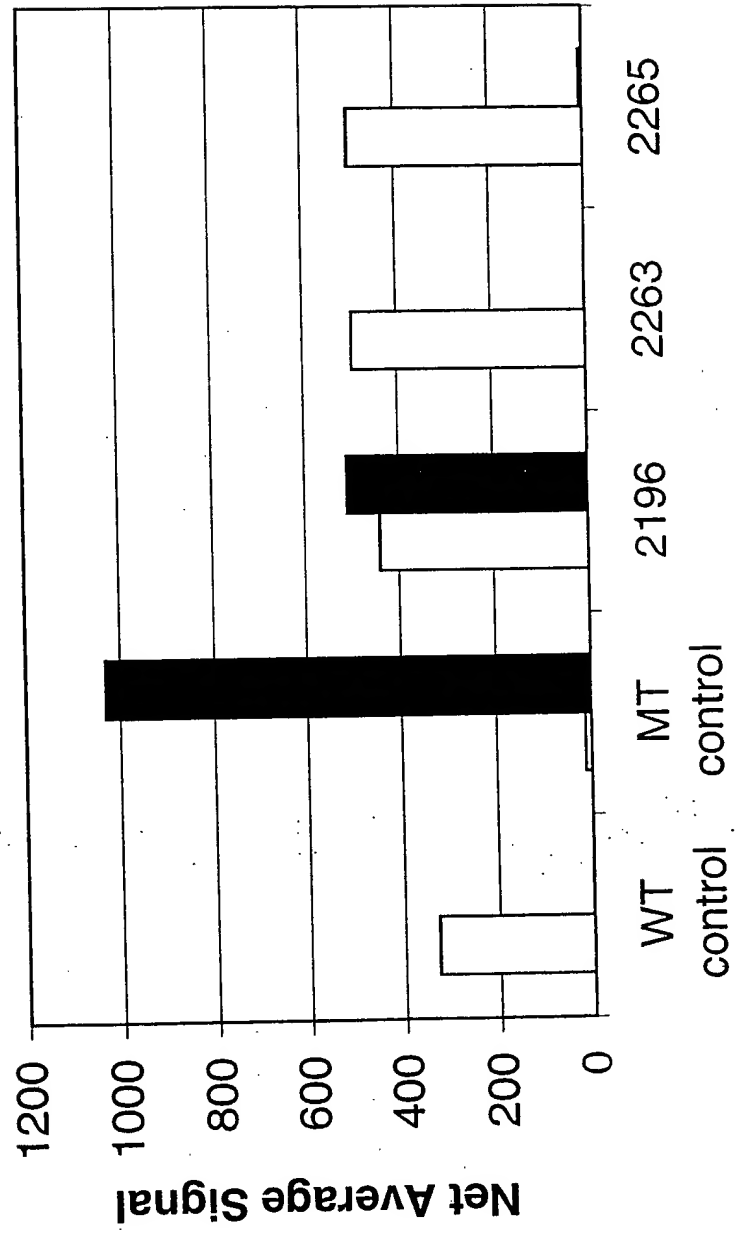


FIGURE 121A

5'-AAGCAGCAGCAGCAGTACAAACCCTTTCTCTAGACAAA
5'-AGATGCCCATTTCTCCAGACCTCAGCCC
3'-GCTACGGGTAAAGAGGTCTGGAGTCGGCATGTTGGGAAAGAGATCTGAAGT-5'

(F) (CY3) CTCC GTCTCGG^T
AAGCAGCAGCAGCAG
UUUCGTCGTCGTGGAGG CAGAGCC^T

FIGURE 121B

5'-AAGCAGCAGCAGGAAACCCCTGTGACAT-3'
 5'-CCATCCAGGGAAGAGTGGCCCTGTTT
 3'-GGGTAGGTCCCTTCTCACCGGACAATCCTTGGGACACTGTAAAGTTT-5'

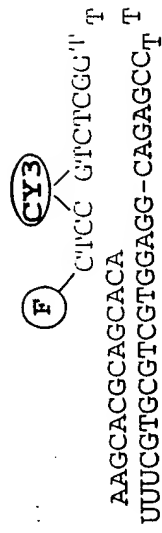


FIGURE 122

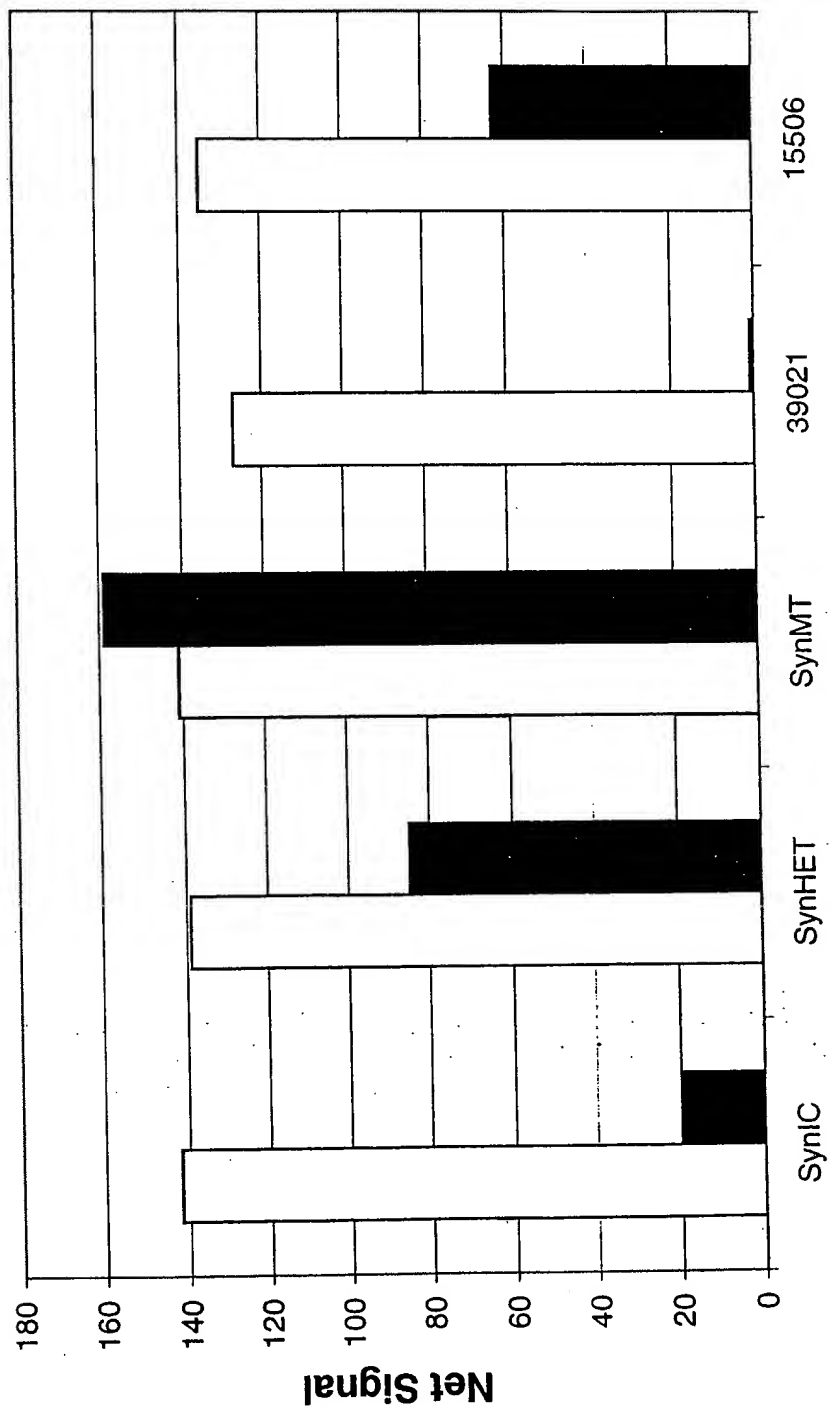


FIGURE 123A

5' - AACGAGGCGCAC CCATGCCCCCTCAAAAC
 5' - GACCCCTGGAGGCTGAACCCCGTCCA
 3' - ATCC'TGGGACCTCCGACTTGGGGCAGGGGTACGGGGAGTTTGGAT-5'

5' - AACGAGGCGCACC
 3' - NH₂ - TTTGCTCCCGTGGGAGCAGAGCC T



FIGURE 123B

5' - AACGAGGCGC^{AC} TCATGCCCCCTCAAAAC
 5' - GACCCCTGGAGGCTGAACCCCGTCCA
 3' - ATCCTGGGACCTCCGACTTGGGCGAGGAGTACGGGGAGTTTGGAT-5'

5' - AACGAGGCGCACT
 3' - NH₂ - TTTGCTCCGCGTGGGAGCAGAGCC T
 (F) (Cy3) CCTCGTCTCGGT T

FIGURE 124

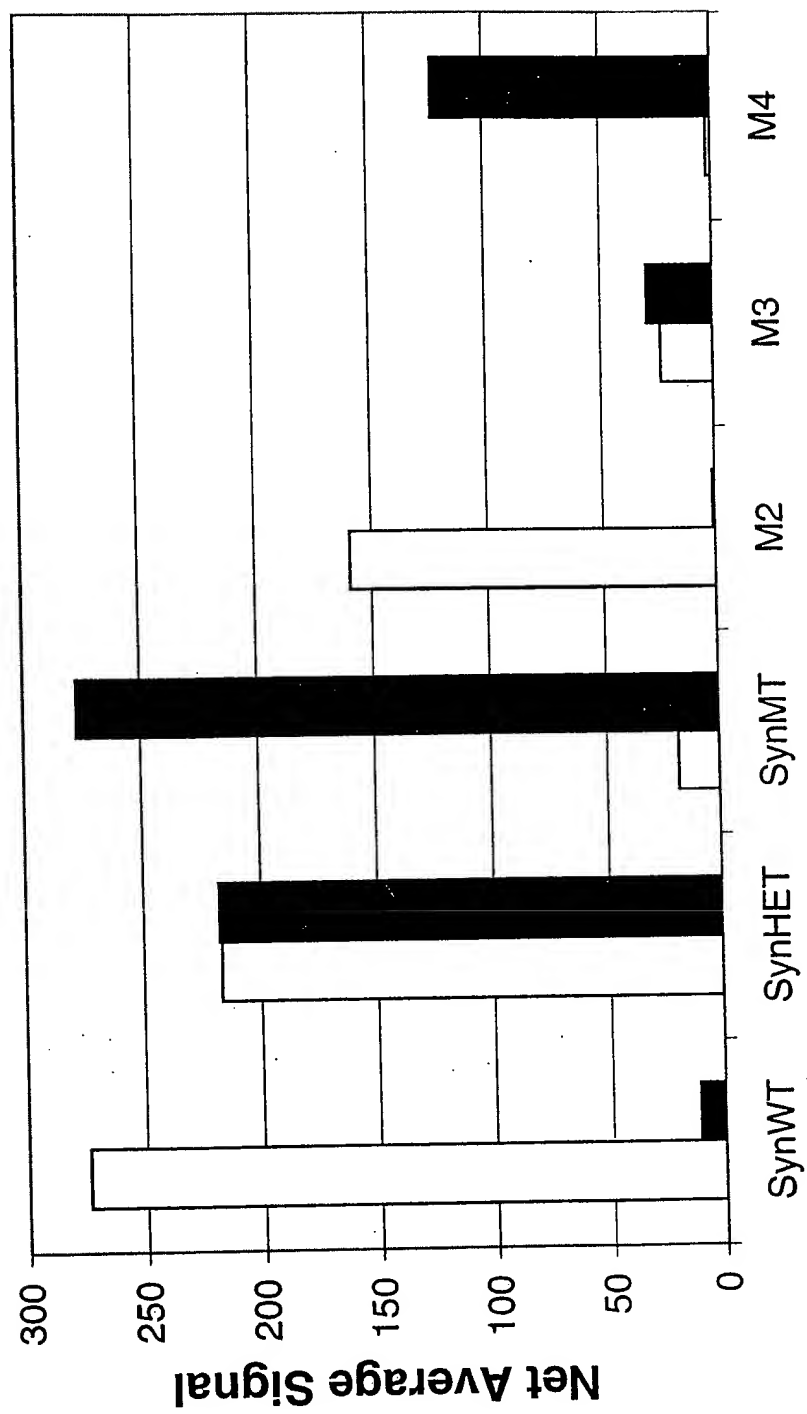


FIGURE 125A

5' - AACGAGGCGCAC GAGGAATACAGGTATTTGTC - NH₃
 5' - TAATCTGTAAGAGCAGATCCCTGGACAGGCC
 3' - AGATTAGACATTCTCGTCTAGGGACCTGTCCGCTCCTTATGTCCATAAACACAGGAA - 5'

5' - AACGAGGCGCACG
 3' - NH₂ - TTTGCTCCGCGTGGGAGCAGAGCC T

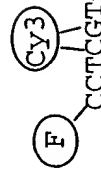


FIGURE 125B

AACGAGGCGCAC AAGGAATACAGGTATTTTGTGTC-NH3
 5'- TAATCTGTAAGAGCAGATCCCCTGGACAGGCC
 3'- AGATTAGACATTCTCGTCTAGGGACCTGTCCGTTCCCTTATGTCCATAAAACAGGAA-5'

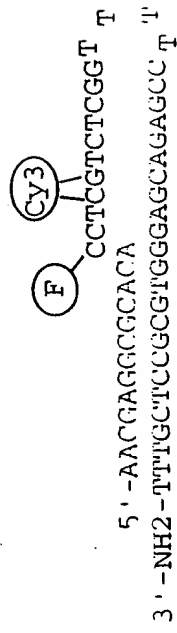


FIGURE 126

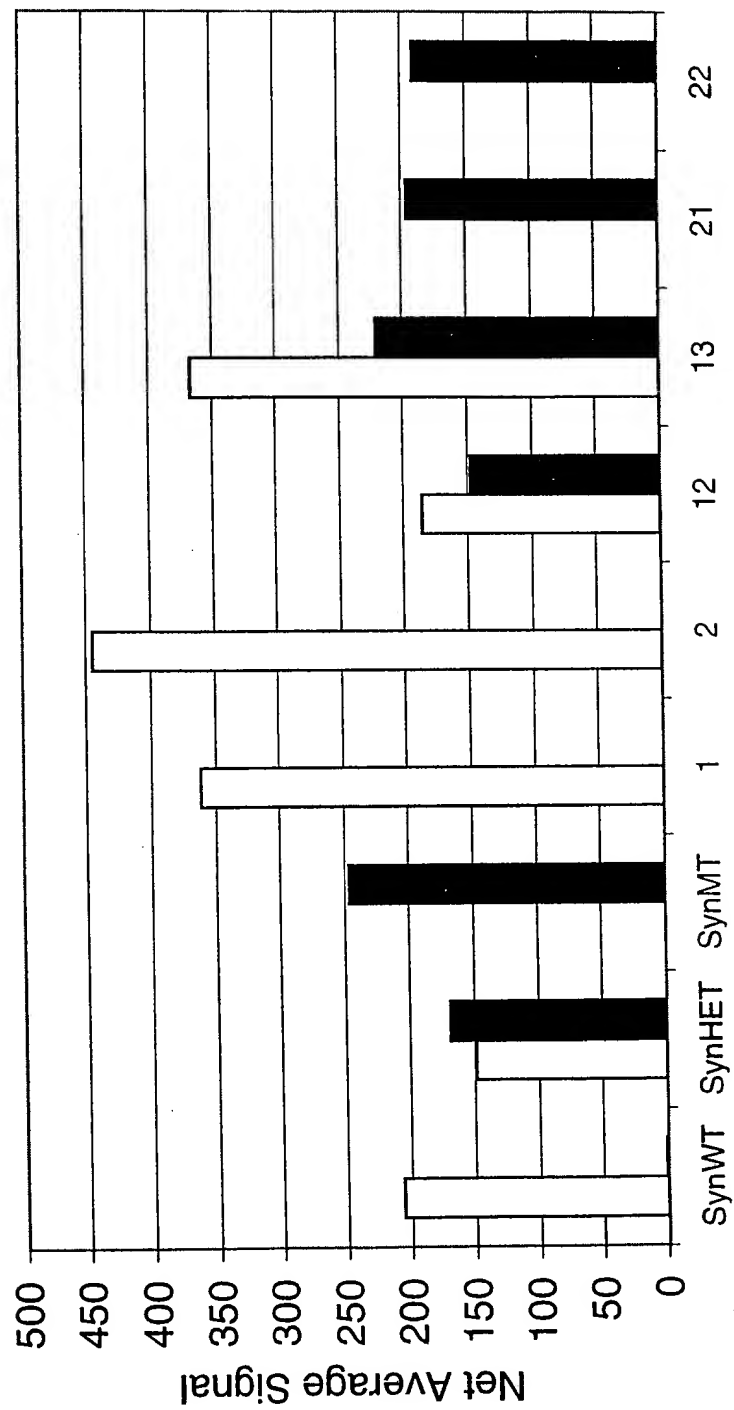


FIGURE 127A

5' - GCGCCGAGG TCTTGGGGTGGTTACAAG-NH₂-3'
 5' - GGTAAGGTTGGCAAAAAGATAAC
 CCATTCCAACCGTTTTTCTATTAGAACCCCAATGTTC-5'

5' - GCGCCGAGGT
 B - GCGCGGCTCCAGAGTCAGAGCC T

(F) (CY3)

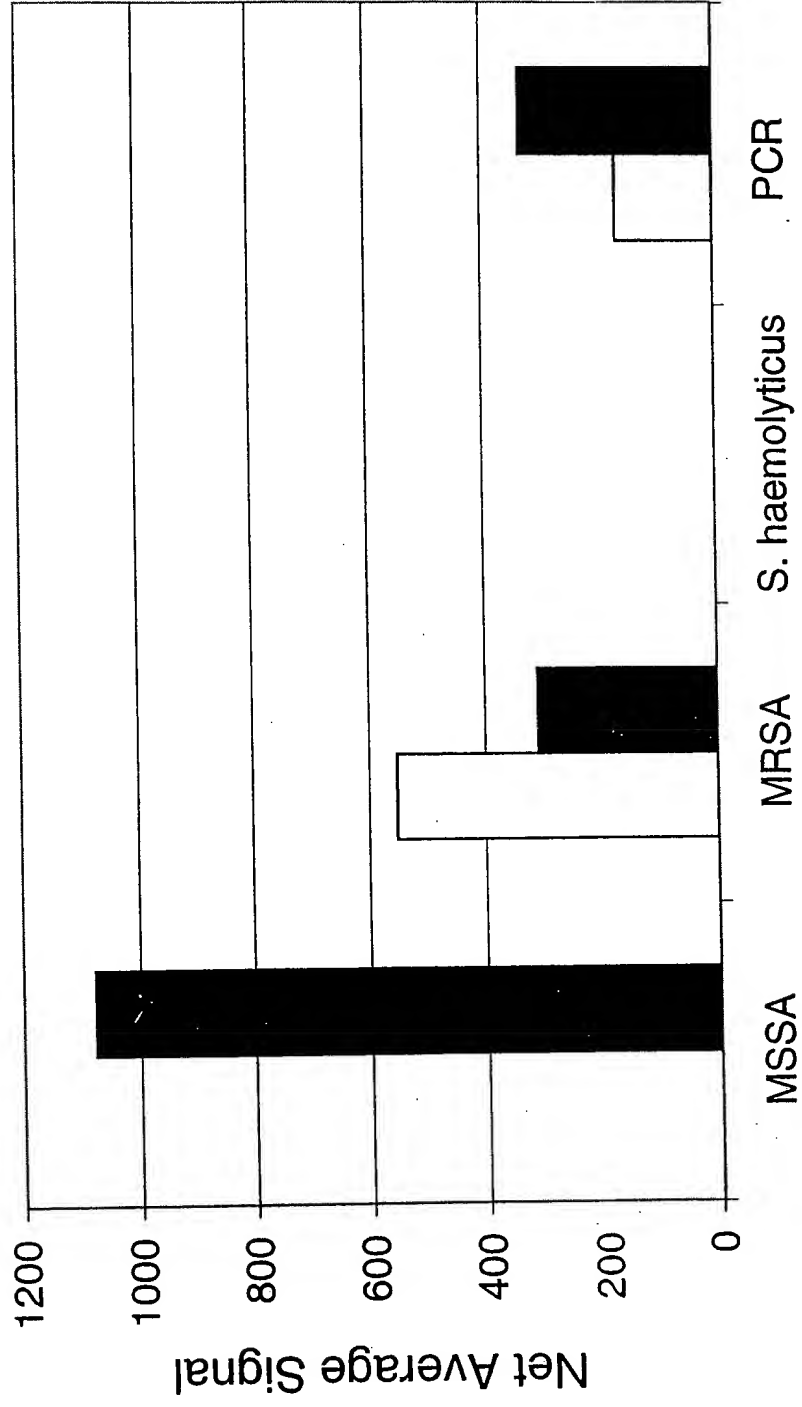
FIGURE 127B

5'-CGCGCCGAGGACACCTTTTATTAGGGTGCTTTGT-NH₂-3'
5'-CACTTGCTTCAGGACCATAATTTCTCTCTC
GTGAACGAAGTCCTGGTATAAAGAGAGATGTGGAATAATCCACGAAACA-5'

5'-CGCGCCGAGGA
B-GCGGGCTCCAGAGTCAGAGCCTT

(F) TCTC GTCTCGG^T T
(CY3)

FIGURE 128



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